

538

Delaval, Jan

From: Roark, Jessica
Sent: Wednesday, October 23, 2002 11:26 AM
To: Delaval, Jan
Subject: 09/728,420

Jan,

Please search, including pending, the following from 09/728,420:

SEQ ID NO:12
SEQ ID NO:7.

Please also align:

SEQ ID NO:17 and SEQ ID NO:18
SEQ ID NO:12 and SEQ ID NO:17
SEQ ID NO:12 and SEQ ID NO:13.

If you can do a pileup of all these sequences, with SEQ ID NO:12 as the reference, that would be great. If you can't do a pileup, then pairwise as indicated.

Results on paper please.

Thanks!

Jessica H. Roark

CM1 8A03
Mailbox 9E12
Art Unit 1644
703 605-1209

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:16:41 ; Search time 29.0328 Seconds
(without alignments)
1231.909 Million cell updates/sec

Title: US-09-728-420C-7

Perfect score: 1687
Sequence: 1 MOLKCPFVSLGTROPVWKK.....RPHRSYTGPKTVQLELTDHA 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
T number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1687	100.0	322	21	AA08725
2	1687	100.0	322	22	AA067711
3	1670	99.0	347	22	AA067712
4	1233.5	73.1	489	22	AA067719
5	600.5	35.6	302	22	AA087395
6	600.5	35.6	344	22	AB010504
7	600.5	35.6	344	22	AA018067
8	599.5	35.5	302	21	AA08729
9	599.5	35.5	302	22	AA067292
10	598.5	35.5	343	22	AB010322
11	598.5	35.5	345	22	AB010502

12	598.5	35.5	345	22	AA018065
13	598.5	35.5	370	22	AA018005
14	594.5	35.2	309	22	AA067713
15	592.5	35.1	516	22	AA00422
16	588.5	34.9	288	21	AA08727
17	569	33.7	239	22	AA00423
18	566.5	33.6	329	21	AA08730
19	558.5	33.1	490	22	AA067718
20	496	29.4	280	21	AA08728
21	249	14.8	316	22	AA00946
22	249	14.8	316	22	AA087394
23	249	14.6	316	20	AA041705
24	247	14.6	316	21	AA044261
25	247	14.6	316	22	AA029050
26	241.5	14.3	340	22	AA00904
27	241.5	14.3	388	22	AA03963
28	241.5	14.3	441	22	AA00905
29	241.5	14.3	534	22	AA00906
30	241.5	14.3	534	22	AA088459
31	241.5	14.3	534	22	AA087250
32	241.5	14.3	1020	22	AA039796
33	241.5	14.3	534	22	AA027249
34	240	14.2	533	22	AA03372
35	236.5	14.0	387	22	AA087415
36	235.5	14.0	469	22	AA041582
37	232.5	13.8	244	22	AA00949
38	227	13.5	216	22	AA00950
39	227	13.5	216	22	AA087417
40	192.5	11.4	133	22	AA067715
41	181	10.7	329	20	AA041076
42	180	10.7	313	19	AA034452
43	179	10.6	358	21	AA04414
44	177	10.5	309	16	AA067988
45	176.5	10.5	250	18	AA014944

ALIGNMENTS

RESULT 1	AA08725
ID	AA08725 standard; Protein; 322 AA.
XX	
AC	AA08725;
XX	
DT	02-JAN-2001 (first entry)
XX	
DE	Amino acid sequence of a murine B7RP1 polypeptide.
XX	
KW	CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
KW	T-lymphocyte activation; type I transmembrane protein; T cell activation;
XX	
XX	T cell proliferation; T-cell mediated disorder.
XX	
OS	Mus sp.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..46
FT	/note= "signal peptide"
FT	47..322
FT	/note= "mature protein"
FT	47..279
FT	/note= "extracellular domain"
FT	280..298
FT	/note= "predicted transmembrane domain"
FT	299..322
FT	/note= "intracellular domain"
XX	
PD	WO200046240-A2.
XX	
PD	10-AUG-2000.
XX	
PF	27-JAN-2000; 2000WO-US01871.
XX	

Human immunoglobulin
Human immunoglobulin
Amino acid sequenc
Human B7-3 protein
Amino acid sequenc
Human B7-3 soluble
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
Human B7-H3 polype
Human gene 2 encod
Human PRO352 prote
Human PRO352 (UNG3
Human PRO polypept
Human B lymphocyte
Human B lymphocyte
Human B lymphocyte
Human B lymphocyte
Human membrane or
Human amyloid prec
Human polypeptide
Human amyloid prec
Human polypeptide
Human gene 2 encod
Human gene 2 encod
Human polypeptide
Human B7-H3 polype
Human B7-H3 polype
Human gene 2 encod
Protein encoded by
Canine B7-2 protel
Rat CD86. Rattus
B7-2-beta 2 microg
Murine B lymphocyt
Chimeric human/por

PR 03-FEB-1999; 9905-0244448.
 PR 08-MAR-1999; 9905-0264527.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Yoshinaga SK;
 XX
 DR WPI: 2000-543476/49.
 DR N-PSDB; AAA64555.
 XX

PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 PT in the treatment, prevention and diagnosis of T cell mediated disorders
 PT
 PS

Claim 12; Fig 2A; 174pp; English.

CC The present sequence represents a B7RP1 (B7 related protein-1)
 CC polypeptide. The specification also describes a CRP1 (CD28 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing, ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX

Sequence 322 AA;

Query Match 100.0%; Score 1687; DB 21; Length 322;
 Best Local Similarity 100.0%; Pred. No. 2.3e-135;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MQLKPCFVSLGTRQPVWKKLHVSSGFFSGIGLFLLLSLCAASAEFEVGMVGSNNYL 60
 QY 61 SCIDPHRRHFNLSGLVYVQIENPEVSVTYLLPYKSPGINDSVSKNRGHSLDSMKGN 120
 DB 61 SCIDPHRRHFNLSGLVYVQIENPEVSVTYLLPYKSPGINDSVSKNRGHSLDSMKGN 120
 QY 121 FSLYLNKNTVPDQTEFTCRVFNMTATELVKILIEEVRLRVANFSTPVISTSDSSNPQOE 180
 DB 121 FSLYLNKNTVPDQTEFTCRVFNMTATELVKILIEEVRLRVANFSTPVISTSDSSNPQOE 180
 QY 181 RITYTCKSKNGYPEPNLWYINTDNLIDTALQNNVTYLNKLGLDVISTRLPMTSRGDV 240
 DB 181 RITYTCKSKNGYPEPNLWYINTDNLIDTALQNNVTYLNKLGLDVISTRLPMTSRGDV 240
 DB 241 LCCVENVALHONITSISQAESEFTGNNTKNPQETHNNELKVLVPLVLAFAAFVSFIITR 300
 QY 301 RTRPHRSYTGPKTVQLELTDHA 322
 DB 301 RTRPHRSYTGPKTVQLELTDHA 322

RESULT 2

AAB67711
 ID AAB67711 standard; Protein; 322 AA.

AC AAB67711;

DT 11-JUN-2001 (first entry)

DE Amino acid sequence of a murine GL50-1.

KW GL50: antigen; antigen presenting cell; T cell proliferation; tumour;
 KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
 KW acquired immune deficiency syndrome; AIDS; vaccine.

OS Mus musculus.
 XX

FH Key location/Qualifiers
 FT Peptide 1..46
 FT /note="Leader sequence"
 FT Domain 47..279
 FT /note="extracellular domain"
 FT Region 280..298
 FT /note="hydrophobic transmembrane region"
 FT Domain 299..322
 FT /note="intracellular cytoplasmic domain"

WO200121796-A2.

PD 29-MAR-2001.

PF 21-SEP-2000; 2000WO-US25892.

PR 21-SEP-1999; 9905-0155043.

PA (GEMV) GENETICS INST INC.

PI Ling V, Dunussi-Joannopoulos K;

DR WPI: 2001-244938/25.

DR N-PSDB; AAF79919.

PT New isolated nucleic acid encoding a GL50 polypeptide for modulating a
 PT immune response and reducing the proliferation of a tumour cell -
 PT

Claim 13; Fig 1; 195pp; English.

CC The present sequence represents a murine GL50-1 polypeptides. GL50
 CC molecules are antigens on the surface of antigen presenting cells,
 CC which costimulate T cell proliferation and bind to costimulatory
 CC receptor ligands on T cells. GL50 modulating agents are used to
 CC modulate an immune response in a subject. GL50 polypeptides are used
 CC to tumour cell costimulation, and to reduce the proliferation of
 CC a tumour cell. Diseases that can be treated using GL50 molecules are
 CC graft-versus-host disease, autoimmune disease, allergies, acquired
 CC immune deficiency syndrome (AIDS), and viral infections. The GL50
 CC molecules can be used in vaccines. GL50 polynucleotides can be used
 CC to locate gene regions associated with genetic disease, in tissue
 CC typing, and in forensic identification of a biological sample.
 XX

Sequence 322 AA;

Query Match 100.0%; Score 1687; DB 22; Length 322;
 Best Local Similarity 100.0%; Pred. No. 2.3e-135;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQLKPCFVSLGTRQPVWKKLHVSSGFFSGIGLFLLLSLCAASAEFEVGMVGSNNYL 60
 DB 1 MQLKPCFVSLGTRQPVWKKLHVSSGFFSGIGLFLLLSLCAASAEFEVGMVGSNNYL 60
 QY 61 SCIDPHRRHFNLSGLVYVQIENPEVSVTYLLPYKSPGINDSVSKNRGHSLDSMKGN 120
 DB 61 SCIDPHRRHFNLSGLVYVQIENPEVSVTYLLPYKSPGINDSVSKNRGHSLDSMKGN 120
 QY 121 FSLYLNKNTVPDQTEFTCRVFNMTATELVKILIEEVRLRVANFSTPVISTSDSSNPQOE 180
 DB 121 FSLYLNKNTVPDQTEFTCRVFNMTATELVKILIEEVRLRVANFSTPVISTSDSSNPQOE 180
 QY 181 RITYTCKSKNGYPEPNLWYINTDNLIDTALQNNVTYLNKLGLDVISTRLPMTSRGDV 240
 DB 181 RITYTCKSKNGYPEPNLWYINTDNLIDTALQNNVTYLNKLGLDVISTRLPMTSRGDV 240
 QY 241 LCCVENVALHONITSISQAESEFTGNNTKNPQETHNNELKVLVPLVLAFAAFVSFIITR 300
 DB 241 LCCVENVALHONITSISQAESEFTGNNTKNPQETHNNELKVLVPLVLAFAAFVSFIITR 300
 QY 301 RTRPHRSYTGPKTVQLELTDHA 322
 DB 301 RTRPHRSYTGPKTVQLELTDHA 322

```

RESULT 3
AAB67712
ID AAB67712 standard; Protein: 347 AA.
XX
XX AAB67712;
AC
XX
XX
DT 11-JUN-2001 (first entry)
XX
XX Amino acid sequence of a murine GL50-2.
DE
XX
XX GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KM graft-versus-host disease; autoimmune disease; allergy; viral infection;
KM acquired immune deficiency syndrome; AIDS; vaccine.
XX
XX Mus musculus.
OS
XX MO200121796-A2.
XX
XX 29-MAR-2001.
PD
XX
XX 21-SEP-2000; 2000WO-US25892.
PE
XX
XX 21-SEP-1999; 99US-0155043.
PR
XX
XX (GEMV ) GENETICS INST INC.
PA
XX
XX Ling V, Dunussi-Joannopoulos K;
PI
XX
XX WPI: 2001-244938/25.
DR
XX
XX N-PSDB; AAF79920.
PT
XX
XX New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT immune response and reducing the proliferation of a tumour cell -
XX
XX
XX Claim 13; Fig 2; 195pp; English.
PS
XX
XX The present sequence represents a murine GL50-2 polypeptides. GL50
CC molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory
CC receptor ligands on T cells. GL50 modulating agents are used to
CC modulate an immune response in a subject. GL50 polypeptides are used
CC to modulate T cell costimulation, and to reduce the proliferation of
CC a tumour cell. Diseases that can be treated using GL50 molecules are
CC graft-versus-host disease, autoimmune disease, allergies, acquired
CC immune deficiency syndrome (AIDS), and viral infections. The GL50
CC molecules can be used in vaccines. GL50 polynucleotides can be used
CC to locate gene regions associated with genetic disease. In tissue
CC typing, and in forensic identification of a biological sample.
XX
XX
SQ Sequence 347 AA:
Query Match 99.0%; Score 1670; DB 22; Length 347;
Best Local Similarity 99.7%; Pred. No. 7.1e-134;
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 MQLKPCFVSLGTROPYWKILHVSQGFSGIGLFLLLSLSCAASAEVEGAMVGSNNVL 60
QY 61 SCIDPHRRHNLGSLYYWQIENPEVSVTYYLYPKSPGINVDSSYNNRGHLSDSKOQN 120
Db 61 SCIDPHRRHNLGSLYYWQIENPEVSVTYYLYPKSPGINVDSSYNNRGHLSDSKOQN 120
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Db 121 FSLYLKAVTPODIOEFCRYFMNTATFLVILKEVYRLRYAANFSPVISTDSSNPGOE 180
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Db 181 RYTCMSKNGYPPENLYWINTDNLIDPALQNNVTYLLKGLGYDYISTLRPLWTSRGDY 240
QY 241 LCCVENALHQNTTSTISQAESFTGNNTKNPOETHNNELKYLVPVLAALAAAFVSFTIYR 300

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Db 241 LCCVENALHQNTTSTISQAESFTGNNTKNPOETHNNELKYLVPVLAALAAAFVSFTIYR 300
QY 301 RTRPHRSYTGPKTYQLELTD 320
Db 301 RTRPHRSYTGPKTYQLELTD 320

RESULT 4
AAB67719
ID AAB67719 standard; Protein: 489 AA.
XX
XX AAB67719;
AC
XX
XX 11-JUN-2001 (first entry)
DT
XX
XX Amino acid sequence of mGL50-mIgG2a fusion protein.
DE
XX
XX GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KM graft-versus-host disease; autoimmune disease; allergy; viral infection;
KM acquired immune deficiency syndrome; AIDS; vaccine.
XX
XX Synthetic.
OS
XX Mus musculus.
XX
XX MO200121796-A2.
XX
XX 29-MAR-2001.
PD
XX
XX 21-SEP-2000; 2000WO-US25892.
PE
XX
XX 21-SEP-1999; 99US-0155043.
PR
XX
XX (GEMV ) GENETICS INST INC.
PA
XX
XX Ling V, Dunussi-Joannopoulos K;
PI
XX
XX WPI: 2001-244938/25.
DR
XX
XX N-PSDB; AAF79942.
PT
XX
XX New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT immune response and reducing the proliferation of a tumour cell -
XX
XX
XX Disclosure: Fig 29B; 195pp; English.
PS
XX
XX The present sequence represents a fusion protein, comprising murine GL50
CC (mGL50) and murine IgG2a (mIgG2A). The fusion protein is used in the
CC course of the invention. The specification describes GL50 polypeptides.
CC GL50 molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory receptor
CC ligands on T cells. GL50 modulating agents are used to modulate an immune
CC costimulation, and to reduce the proliferation of a tumour cell. Diseases
CC that can be treated using GL50 molecules are graft-versus-host disease,
CC autoimmune disease, allergies, acquired immune deficiency syndrome
CC (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
CC GL50 polynucleotides can be used to locate gene regions associated with
CC genetic disease, in tissue typing, and in forensic identification of a
CC biological sample.
XX
XX
SQ Sequence 489 AA:
Query Match 73.1%; Score 1233.5; DB 22; Length 489;
Best Local Similarity 96.4%; Pred. No. 1.6e-96;
Matches 238; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
QY 31 LGLFLLLSLSCAASAEVEGAMVGSNNVLSCIDPHRRHNLGSLYYWQIENPEVSVTY 90
Db 11 LSLVALLFP-SMAEMTEVGAMVGSNNVLSCIDPHRRHNLGSLYYWQIENPEVSVTY 69
QY 91 YLPKSPGINVDSSYNNRGHLSDSKOQNFSLYLNVTPODIOEFCRYFMNTATFLVK 150
Db 70 YLPKSPGINVDSSYNNRGHLSDSKOQNFSLYLNVTPODIOEFCRYFMNTATFLVK 129

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QY	92	LPKKSGIWDVSDYKRNKRLSDSMKQNFSLYLNKVTPODTQETCFVFMNATFELVKI	151
Db	67	IQNSLSLEWVDSRYRNRALMSAPAGMLRGDFSLRFLFWPVPQDDQKFCFLV-LSQSLGFOEV	125
QY	152	LEEVLRLVAAAFSTPVIISTSDSSNPGQ-ERYTYCKMSKGYEPNNYINTDNSLIDPA	210
Db	126	LSEVYTLHNAANFSPVVSAPHS--PSQDELFTFTCTISNGYRPNNYWNKTDNSLIDQA	183
QY	211	LQNTVYLNKGLDYIVISTRLPWTSGRDVLCVENVALHONITSISQASEFTGNN---	266
Db	184	LQNDVFLMLMRLGLYVVSVLRIATRPVNIIGCIEVLLQMLTVGSG---TGNDIGER	239
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DT	10-JAN-2002	(first entry)	
XX	Human CDNA SEQ ID NO: 812.		
DE	Human CDNA SEQ ID NO: 812.		
XX	Human: gene therapy; neural disorder; immune system disorder;		
KW	muscular disorder; reproductive disorder; gastrointestinal disorder;		
KW	pulmonary disorder; cardiovascular disorder; renal disorder;		
KW	proliferative disorder; inflammation.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	WO200154474-A2.		
PN	WO200154474-A2.		
XX	02-AUG-2001.		
PD	02-AUG-2001.		
XX	17-JAN-2001; 2001MO-US01349.		
XX	17-JAN-2001; 2001MO-US01349.		

Gencore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:28:41 ; Search time 12.6689 Seconds
(without alignments)
620.817 Million cell updates/sec

Title: US-09-728-420C-7
Perfect score: 1687
Sequence: 1 MQLKCPYSLGTROPVKK.....RPHSYGPKTVQLDLDDHA 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues
T number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	175.5	10.4	329	2	Sequence 2, Appl1
4	175.5	10.4	329	3	Sequence 2, Appl1
5	175.5	10.4	329	4	Sequence 2, Appl1
6	175.5	10.4	329	4	Sequence 2, Appl1
7	175.5	10.4	329	4	Sequence 2, Appl1
8	175.5	10.4	329	4	Sequence 2, Appl1
9	175.5	10.4	329	5	Sequence 2, Appl1
10	175.5	10.4	309	2	Sequence 4, Appl1
11	175.5	10.4	309	3	Sequence 23, Appl1
12	175.5	10.4	309	4	Sequence 23, Appl1
13	175.5	10.4	309	4	Sequence 21, Appl1
14	175.5	10.4	309	4	Sequence 21, Appl1
15	175.5	10.4	309	5	Sequence 21, Appl1
16	175.5	10.4	314	4	Sequence 13, Appl1
17	175.5	10.4	314	4	Sequence 13, Appl1
18	175.5	10.4	314	5	Sequence 13, Appl1
19	175.5	10.4	314	5	Sequence 13, Appl1
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28	160	9.5	288	4	Sequence 19, Appl1
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33	151.5	9.0	589	2	Sequence 1, Appl1
34	150	8.9	208	4	Sequence 36, Appl1
35	144.5	8.6	306	4	Sequence 17, Appl1
36	144.5	8.6	306	4	Sequence 17, Appl1
37	144.5	8.6	306	5	Sequence 17, Appl1
38	143.5	8.5	306	2	Sequence 8, Appl1
39	143.5	8.5	306	2	Sequence 8, Appl1
40	143.5	8.5	306	2	Sequence 8, Appl1
41	143.5	8.5	306	3	Sequence 25, Appl1
42	143.5	8.5	306	3	Sequence 4, Appl1
43	143.5	8.5	306	3	Sequence 31, Appl1
44	143.5	8.5	306	4	Sequence 31, Appl1
45	143.5	8.5	306	4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
PCT-US94-09642-2
Sequence 2, Application PC/TUS9409642

GENERAL INFORMATION:

APPLICANT: Purified Mammalian CTLA-4 Binding
TITLE OF INVENTION: Protein and Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering-Plough Corporation, M-3-W
STREET: One Giralda Farms

CITY: Madison
STATE: New Jersey
COUNTRY: USA

ZIP: 07940-1000

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh IIcx
OPERATING SYSTEM: System Software 7.1

SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09642
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/120,606
FILING DATE: 13-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,882

FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:

NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895

REFERENCE/DOCKET NUMBER: DX0390K1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-822-7398
TELEFAX: 201-822-7039

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 323 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

PCT-US94-09642-2
Query Match

Best Local Similarity 24.8%; Pred. No. 7.9e-08;
Matches 75; Conservative 51; Mismatches 142; Indels 35; Gaps 11;

QY 30 GGLFLLLSLICASALETEGVAMGWNVLSCIDPHRRHNLGSLVYVWQIENPEVSVT 89

Db 2 GLSNILFVMAFLISGAAPLKIQAIFNETADLPCOFANSQMSLSLVVFQDQENLYLNE 61
QY 90 YLLPYKSPGINVDSSYKNGHLSLDSMKOGNFSLYLKNVTPODTQEFYCFRPMWTATELV 149
Db 62 YVLG-KERKDSVHSKMYGRTSPDSDS-----WTLRLHNLQIKDKGLYCITIIHKKPTGMI 115
QY 150 KILEEVLRLVAANFSTPYISTSDSSNPGQERTYTCMSKNGYPEP-NLWYINTDNLIT- 207
Db 116 RIHQMSLSLVANFSQPELVPISNITENYINLTCSIHGYEPKMSVLLRTKNSTIE 175
QY 208 -DTALONNTYVLYLNGLYDVISTRLFPW---TSRGDVLCCVENVALHQNTISISQAESFT 263
Db 176 YDGMOKSOD--NVTLEYDVISISVSFPDVTSMNTEICILET-----DKTRLSSPESI- 228
QY 264 GNNTKNPOETHNNELKVLVPLAVLAANAFAVSFIY-----RTRPHRSY-TGPKYV 314
Db 229 --ELEDPPPPDH-----IPWITAVLPVILICVWFCLIMKWKKKRPRNSYKCGTNTM 281
315 QLE 317
282 ERE 284

RESULT 2

US-08-456-104-2
; Sequence 2, Application US/08456104

; Patent No. 5861310

; GENERAL INFORMATION:

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee M.

; APPLICANT: Gray, Gary S.

; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/456,104

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/101,624;

; FILING DATE: 26-JUL-1993;

; APPLICATION NUMBER: 08/109,393;

; APPLICATION NUMBER: 19-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: RPI-008

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 329 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-456-104-2

QY 30 GIGLFLILLSSICAASTETEVGAMGNNVLSCIDPHRRHFLSLYYVNOLENPEVSVT 89
Db 8 GLSNILFVMAFLISGAAPLKIQAIFNETADLPCOFANSQMSLSLVVFQDQENLYLNE 67
QY 90 YLLPYKSPGINVDSSYKNGHLSLDSMKOGNFSLYLKNVTPODTQEFYCFRPMWTATELV 149
Db 68 YVLG-KERKDSVHSKMYGRTSPDSDS-----WTLRLHNLQIKDKGLYCITIIHKKPTGMI 121
QY 150 KILEEVLRLVAANFSTPYISTSDSSNPGQERTYTCMSKNGYPEP-NLWYINTDNLIT- 207
Db 122 RIHQMSLSLVANFSQPELVPISNITENYINLTCSIHGYEPKMSVLLRTKNSTIE 181
QY 208 -DTALONNTYVLYLNGLYDVISTRLFPW---TSRGDVLCCVENVALHQNTISISQAESFT 263
Db 182 YDGMOKSOD--NVTLEYDVISISVSFPDVTSMNTEICILET-----DKTRLSSPESI- 234
QY 264 GNNTKNPOETHNNELKVLVPLAVLAANAFAVSFIY-----RTRPHRSY-TGPKYV 314
Db 235 --ELEDPPPPDH-----IPWITAVLPVILICVWFCLIMKWKKKRPRNSYKCGTNTM 287
315 QLE 317
288 ERE 290

RESULT 3

US-08-101-624-2

; Sequence 2, Application US/08101624

; Patent No. 5942607

; GENERAL INFORMATION:

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee M.

; APPLICANT: Gray, Gary S.

; TITLE OF INVENTION: NO. 5942607/EL CTLA4/CD28 Ligands and

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/101,624

; FILING DATE: 26-JUL-1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: RPI-004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 329 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-101-624-2

Query Match 10.4%; Score 175.5; DB 2; Length 329;
Best Local Similarity 24.8%; Pred. No. 8,le-08;
Matches 75; Conservative 51; Mismatches 142; Indels 35; Gaps 11;

Query Match 10.4%; Score 175.5; DB 2; Length 329;
Best Local Similarity 24.8%; Pred. No. 8,le-08;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:27:51 ; Search time 16.3639 Seconds
(without alignments)
1890.790 Million cell updates/sec

Title: US-09-728-420C-7
Perfect score: 1687
Sequence: 1 MOLKCPGFVSLGTRQFPWK.....RPHRSTYGPKTQLELTDDHA 322

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
T number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	10.9	330	2	146691
2	177	10.5	299	2	146690
3	176.5	10.5	275	2	JC7604
4	175.5	10.4	329	1	A48754
5	175	10.4	309	2	149522
6	164	9.7	321	2	154766
7	160	9.5	288	2	A45803
8	151.5	9.0	526	2	S70587
9	146	8.7	289	2	G00031
10	145.5	8.6	487	2	S65133
11	145	8.5	526	2	A37821
12	144	8.5	309	2	149503
13	129	7.6	233	2	S29577
14	128.5	7.6	299	2	S56749
15	121	7.2	531	2	S06016
16	121	7.2	537	2	149769
17	120	7.1	537	2	A45815
18	119.5	7.1	646	2	138049
19	117.5	7.0	391	2	T09058
20	115.5	6.8	3707	2	S18252
21	115	6.8	662	2	T16525
22	114.5	6.8	549	2	S04845
23	114	6.8	1348	2	S51656
24	113	6.7	521	2	S34338
25	113	6.7	1106	1	PFH0GB
26	113	6.7	6642	1	T29757
27	112.5	6.7	509	2	JC5288
28	112.5	6.7	513	2	JC5289
29	112	6.6	503	2	JC5287

30	111.5	6.6	167	2	S29579	Ig light chain - r
31	111.5	6.6	1098	1	PFMR8B	platelet-derived g
32	111	6.6	583	2	I39428	album - human
33	110.5	6.6	588	2	JH0506	adhesion molecule
34	110.5	6.6	588	2	A45254	surface glycoprote
35	110	6.5	247	2	A55717	myelin/oligodentro
36	109.5	6.5	521	2	JC1508	biliary glycoprote
37	108	6.4	241	2	S69131	Ig heavy chain (DO
38	108	6.4	523	2	I50478	neurotin - goldfis
39	108	6.4	526	1	A32164	biliary glycoprote
40	107.5	6.4	587	2	JH0464	DM-GRASP precursor
41	106.5	6.3	588	2	I37202	B-CAM protein - hu
42	106	6.3	416	1	A42879	advanced glycosyla
43	106	6.3	1259	2	S36126	neural cell adhesi
44	105.5	6.3	228	2	S29575	Ig light chain - r
45	105.5	6.3	1694	2	S50065	staloadesin - mou

ALIGNMENTS

RESULT 1
146691
CD86 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C:Accession: 146691
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole
A:Reference number: 146689; MUID:95369849
A:Accession: 146691
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-330 <IS0>
A:Cross-references: GB:D49842; NID:9755098; PIDN:BA08642.1; PID:9755099
C:Superfamily: B7-2 antigen

Query Match 10.9%; Score 184; DB 2; Length 330;
Best Local Similarity 23.8%; Pred. No. 1.9e-06;
Matches 70; Conservative 53; Mismatches 137; Indels 34; Gaps 9;

Qy	23	VSSGFFSGLGIFLLLSLCAASAEVEGAMVGSNVYLSGIDPHRRHFNLSGLYVMOIE 82
Db	1	MDACITGLSVTFVFMALLSGAASLRIOAYFNKTADLPQFTNSOSRSLSELVFWODQ 60

Qy	83	NPEYSVTVYLYPKSPGINVDSSYKNRGHLSDSMKQGNFSLYLKNYTPDPTQFTGRVFM 142
Db	61	ERLVLYELFLGREKPD-NVDPKTYIGR-----TSFDQSMNLOLHNVOIKKKGYQCFVHH 114

Qy	143	NTATELVKILIEEVRRLVNAANFSTPVISTSDSNPGQERTYTCMSKNGYEP-NLWIINT 201
Db	115	RGAGGLVPIYQMSNELSVLANFTQPEITLLSNITRNSAINLTCSSVOGYDEPKRMFEVLK 174

Qy	202	TDNS-----LIDFALDNNTYVYLNKLGIVYISTRLRPMWS--RGDLGVGCV---ENVALH 250
Db	175	TENATFEYDGVIEKSQONVT-----GLYNTISISGSTFESDDIRNATITYVLQTESLEY 228

Qy	251	QNITSISOAESFTGNMTKNPDETHNNELKLVPLVLAIAAAAFVSFT-IYRRT 303
Db	229	SQHPPIYPAD-----PYVPEKPRMIAAVALTLIVYCGIVLFLTLMKRKK 273

RESULT 2
146690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: 146690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole
A:Reference number: 146689; MUID:95369849

A:Accession: I46690
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-299 <ISO>
 A:Cross-references: GB:D49843; NID:9755096; PIDN:BA008643.1; PID:9755097
 C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 10.5%; Score 177; DB 2; Length 299;
 Best Local Similarity 25.8%; Pred. No. 5.7e-06;
 Matches 77; Conservative 42; Mismatches 120; Indels 60; Gaps 11;

QY 35 LLLSLCAASAEVEGAMGVNSVLSG-----IDPHRRHFMISGLYVWQIENPEVSVT 89
 DB 22 LLAALAIHSSSGISQVTKSKEMALSCDYNISID-----ELARRIYVQKQOV--- 72
 QY 90 YLIPYKSPGINVDSSYKNGHLSIDSMKGNFSLYKNTVPDQTEGTCRFVMTATELV 149
 DB 73 --LSISGOVEWPEYKKNTPFDIIN---NLSMLLALRLSDKGTTCVQKNENGSR 126
 150 KILEEYVRLVAAVFSTPVISTDSSNPGQERTYTCMSKNGYPEPMLYV-----IN 200
 127 REHLTSVTLISRADFPVPSITDIGHDDPNVKR-IRCSASGCFPEPRPLAMDEGEELNAV 185
 QY 201 TTPNSLIDPALQNTYVYKLGIDYISTRLRPMTSRGDVLCCEVNAALHONTISQAE 260
 DB 186 TTVDDQDLDE-----LYSVSELDEFNVTNNHSHVCLIKYGEI-----SVSOIF 228
 QY 261 SFGNNTKPNQETHNELK--VLVPLVLAALAAAFVSFI-----YRRTRPHRSYTG 310
 DB 229 PW-----SKRQEPPIQGLPFVWYIIPVSGALVLTAVVLYCLACRHVARKKTRRNEETWG 283

RESULT 3

CD86 spliced variant CD86 deltaTM isoform - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
 C:Accession: J07604
 R:Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.
 Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
 A:Title: Identification of an alternatively spliced variant of human CD86 mRNA.
 A:Reference number: J07604; MUID:21092744; PMID:11162656
 A:Accession: J07604
 A:Molecule type: mRNA
 A:Residues: 1-275 <MAC>
 C:Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
 C:Genetics:
 A:Gene: cd86deltaTM
 Keywords: immune response

Query Match 10.5%; Score 176.5; DB 2; Length 275;
 Best Local Similarity 26.6%; Pred. No. 5.6e-06;
 Matches 73; Conservative 44; Mismatches 136; Indels 21; Gaps 8;

QY 30 GLGLFLLLSLCAASAEVEGAMGVNSVLSCTIDPHRRHFMISGLYVWQIENPEVSVT 89
 DB 2 GLSNILFVMAFLISGAAPLKIQAVFNETADLPQOPANSQNSLSLVYFWDQDENLVNE 61
 QY 90 YLIPYKSPGINVDSSYKNGHLSIDSMKGNFSLYKNTVPDQTEGTCRFVMTATELV 149
 DB 62 YVLG-KEKFDVSHKYMGTSPDS-----WTLRLHLNLIQIKDKGLYQCIHHKKPTGMI 115
 QY 150 KILEEYVRLVAAVFSTPVISTDSSNPGQERTYTCMSKNGYPEP-NLYWINTDMSLI- 207
 DB 116 RIHOMNSELVLANFSOPEIYVPSNITEENVYINLTCSIHGPEPKKMSVLLRTKNSITE 175
 QY 208 -PTAQNNTYVYKLGIDYISTRLRPW---TSRGDVLCCEVNAALHONTISQAESEFT 263
 DB 176 YDGMQKSD--NVTGLYDVISISVSFPDYTSNMTIFCILET-----DKTRLSSPFSI 228

QY 264 GNNTKPNQETHNELK--VLVPLVLAALAAAFVS 295
 DB 223 GNTMERESSEOTKKREKIHIPENSDERQVFKS 262

RESULT 4

A48754
 B7-2 antigen - human
 N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A48754; S39055
 R:Freeman, G.V.; Gridben, T.G.; Bousset, V.A.; Ng, J.W.; Restifo Jr., V.A.; Lombard
 Science 262, 909-911, 1993
 A:Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell pr
 A:Reference number: A48754; MUID:94053735
 A:Accession: A48754

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-329 <FRET>
 A:Cross-references: GB:D25259; NID:9416368; PIDN:AAA58389.1; PID:9416369
 A:Note: It is uncertain whether Met-1 or Met-7 is the initiator
 R:Aizuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lander, L.L.; Somoza,
 Nature 366, 76-79, 1993
 A:Title: B70 antigen is a second ligand for CTLA-4 and CD28.
 A:Reference number: S39055; MUID:94050123
 A:Accession: S39055
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 7-329 <AZU>
 A:Cross-references: GB:U04343; NID:9439838; PIDN:AA03814.1; PID:9439839
 C:Genetics:
 A:Gene: GDB:CD86; CD28LG2
 A:Cross-references: GDB:433597; OMIM:601020
 A:Map position: 3q13.3-3q21
 C:Superfamily: B7-2 antigen
 C:Keywords: glycoprotein

Query Match 10.4%; Score 175.5; DB 1; Length 329;
 Best Local Similarity 24.8%; Pred. No. 8.4e-06;
 Matches 75; Conservative 51; Mismatches 142; Indels 35; Gaps 11;

QY 30 GLGLFLLLSLCAASAEVEGAMGVNSVLSCTIDPHRRHFMISGLYVWQIENPEVSVT 89
 DB 8 GLSNILFVMAFLISGAAPLKIQAVFNETADLPQOPANSQNSLSLVYFWDQDENLVNE 67
 QY 90 YLIPYKSPGINVDSSYKNGHLSIDSMKGNFSLYKNTVPDQTEGTCRFVMTATELV 149
 DB 68 YVLG-KEKFDVSHKYMGTSPDS-----WTLRLHLNLIQIKDKGLYQCIHHKKPTGMI 121
 QY 150 KILEEYVRLVAAVFSTPVISTDSSNPGQERTYTCMSKNGYPEP-NLYWINTDMSLI- 207
 DB 122 RIHOMNSELVLANFSOPEIYVPSNITEENVYINLTCSIHGPEPKKMSVLLRTKNSITE 181
 QY 208 -PTAQNNTYVYKLGIDYISTRLRPW---TSRGDVLCCEVNAALHONTISQAESEFT 263
 DB 182 YDGMQKSD--NVTGLYDVISISVSFPDYTSNMTIFCILET-----DKTRLSSPFSI- 234
 QY 264 GNNTKPNQETHNELKVLVPLVLAALAAAFVSFIY-----RRTPRRSY-TGPKTV 314
 DB 235 --ELEDDQPPDH-----IPWITAVLPTVILICVWVCLIMKKKKKRRPNSYKCGTNNM 287
 QY 315 QLE 317
 DB 288 ERE 290

RESULT 5

I49522
 gene B7-2 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
 C:Accession: I49522
 R:Freeman, G.V.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gridben, J.G.; Ng, J.W.; Kim
 J. Exp. Med. 178, 2185-2192, 1993
 A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:23:41 ; Search time 9.50164 Seconds
(without alignments)
1312.163 Million cell updates/sec

Title: US-09-728-420c-7
Perfect score: 1687
Sequence: 1 MOLKCPFVSLGTROPVWK.....RPHSYTGPKTVQLELDHA 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1687	100.0	322	1	ICOL_MOUSE
2	599.5	35.5	302	1	ICOL_HUMAN
3	184	10.9	330	1	CD86_RABBIT
4	177	10.5	299	1	CD80_RABBIT
5	175.5	10.4	329	1	CD86_HUMAN
6	175	10.4	309	1	CD86_MOUSE
7	162	9.6	524	1	BUTY_MOUSE
8	160	9.5	288	1	CD80_HUMAN
9	151.5	9.0	526	1	BUTY_HUMAN
10	145	8.6	526	1	BUTY_BOVIN
11	144.5	8.6	306	1	CD80_MOUSE
12	128.5	7.6	299	1	JAML_HUMAN
13	121	7.2	537	1	ICAM_MOUSE
14	121	7.2	583	1	CD16_MOUSE
15	119.5	7.1	298	1	JAM2_HUMAN
16	119.5	7.1	646	1	MU18_HUMAN
17	115.5	6.8	3707	1	PGBM_MOUSE
18	114	6.8	1348	1	VGR2_COTJA
19	113	6.7	1106	1	PGDR_HUMAN
20	111.5	6.6	555	1	CD16_CARAU
21	111.5	6.6	1098	1	PGDR_MOUSE
22	111	6.6	583	1	CD16_HUMAN
23	110.5	6.6	246	1	MOS_MOUSE
24	110.5	6.6	588	1	CD16_CHICK
25	109.5	6.5	521	1	CEAL_MOUSE
26	108	6.4	319	1	A33_HUMAN
27	108	6.4	526	1	CEAL_HUMAN
28	106	6.3	416	1	RAGE_BOVIN
29	106	6.3	1259	1	CAML_RAT
30	105.5	6.3	298	1	JAML_BOVIN
31	105.5	6.3	1694	1	SN_MOUSE
32	105	6.2	245	1	MOS_RAT
33	104.5	6.2	313	1	HEMA_VARV

34	104.5	6.2	421	1	EPG_MOUSE	P06336	mus musculus
35	104.5	6.2	569	1	TACT_HUMAN	P40200	homo sapien
36	104.5	6.2	730	1	ERG7_YEAST	P38604	saccharomyc
37	102.5	6.1	310	1	HEMA_RACVI	000716	raccoon pox
38	102.5	6.1	481	1	MUCM_ICMPU	P23735	ictalurus pox
39	102	6.0	1709	1	SN_HUMAN	09b222	homo sapien
40	101.5	6.0	459	1	CD4_RABBIT	P46630	oryctolagus
41	101.5	6.0	1257	1	CAML_HUMAN	P32004	homo sapien
42	101	6.0	315	1	HEMA_VACCI	P08714	vaccinia vl
43	100	5.9	246	1	MOS_BOVIN	P55803	bos taurus
44	100	5.9	564	1	CD16_BRARE	090460	brachydanio
45	99.5	5.9	628	1	LD_HUMAN	P50895	homo sapien

ALIGNMENTS

RESULT 1
ICOL_MOUSE
ID ICOL_MOUSE STANDARD: PRT: 322 AA.
AC Q9JHJ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
DE (B7-related protein-1) (B7Rp-1) (LICOS).
GN ICOSL OR B7H2 OR B7RPL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RP TISSUE=Lymphocytes;
RC MEDLINE=20083495; PubMed=10617205;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,
RA Elliott G.S., Hui A., McCabe S.M., Scully S., Shadlun A.,
RA Shalke C.L., Van G., Mak T.W., Senaldi G.;
RT "T-cell co-stimulation through B7Rp-1 and ICOS.";
RN Nature 402:827-832(1999).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Thymus;
RC MEDLINE=20015817; PubMed=10549624;
RA Swallow M.M., Wallin J.J., Sha W.C.;
RT "B7, a novel costimulatory homolog of B7.1 and B7.2, is induced by
RT TNFalpha.";
RN Immunity 11:423-432(1999).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP STRAIN=C3H/HeJ; TISSUE=fetal thymus;
RC MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA Leonard J.P., Hunter S.E., Zoliner R., Thomas J.L., Miyashiro J.S.,
RA Jacobs K.A., Collins M.;
RT "Identification of G150, a novel B7-like protein that functionally
RT binds to ICOS receptor.";
RN J. Immunol. 164:1653-1657(2000).
[4]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE=peripheral blood lymphocytes;
RC MEDLINE=21286479; PubMed=11390480;
RA Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F.,
RA Collins M.;
RT "Differential expression of inducible costimulator-ligand splice
RT variants: lymphoid regulation of mouse g150-b and human g150
RT molecules.";
RN J. Immunol. 166:7300-7308(2001).
[5]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Ling V., Dunussi-Joannopoulos K.;

RT "G150 molecules and uses therefor.";
 RL Patent number WO0121796, 29-MAR-2001.
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS. AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
 CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
 CC TH2 PHENOTYPE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
 CC (PARTICULARLY IN THE CORTX AND IN BOTH PRIMARY AND SECONDARY
 CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND Peyer's
 CC PATCHES (MOSTLY IN THE FOLLICLES). LOWER LEVELS IN MANY
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
 CC CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
 CC -1- DEVELOPMENTAL STAGE: DETECTED EARLY IN EMBRYONISTS; IN THE YOLK
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
 CC 14.5 DPC.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -----
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 CC -----
 CC EMBL: AF216747; AAF45149.1; -
 CC EMBL: AF199027; AAF34738.1; -
 CC EMBL: AX100591; CAC36463.1; -
 CC EMBL: AX100593; CAC36464.1; -
 CC EMBL: AF394451; AAK77544.1; -
 CC MGD: MGI:1354701; Icosl.
 CC DR InterPro: IPR003599; IG.
 CC DR InterPro: IPR003006; IG_MHC.
 CC DR InterPro: IPR003600; IG_Like.
 CC Pfam: PF00047; Ig_1.
 CC SMART: SM00409; IG_1.
 CC SMART: SM00410; IG_Like; 1.
 CC DR B-cell activation; Immune response; Glycoprotein;
 CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 CC Alternative splicing.
 CC -----
 CC FT SIGNAL 1 46 BY SIMILARITY.
 CC FT CHAIN 47 322 ICOS LIGAND.
 CC FT DOMAIN 47 277 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 278 298 POTENTIAL.
 CC FT DOMAIN 299 322 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 322 322 IG-LIKE V-TYPE DOMAIN.
 CC FT DOMAIN 178 250 IG-LIKE C2-TYPE DOMAIN.
 CC FT DOMAIN 31 38 POLY-LEU.
 CC FT DOMAIN 289 292 POLY-ALA.
 CC FT DISULFID 62 138 POTENTIAL.
 CC FT DISULFID 185 243 POTENTIAL.
 CC FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPL 321 322 HA -> TWAPVYQDYLIPIRLMSPCLKTGLP (IN

FT ISOFORM 2).
 FT CONFLICT 237 237 R -> H (IN REF. 4 AND 5; CAC36464).
 FT SEQUENCE 322 AA: 35960 MW: 550CBAA4AD12B47E6 CRC64;
 SQ
 Query Match 100.0%; Score 1687; DB 1; Length 322;
 Best local similarity 100.0%; Pred. No. 3, 8e-129;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQMKPCFVSGTGPVWKRIHVSSGFFSGIGLELLLSLCAASATFVGAWGSAVVL 60
 DB 1 MQLKCPFCVSLGTROPVWKRLHVSSGFFSGIGLELLLSLCAASATFVGAWGSAVVL 60
 QY 61 SCIPRRHFMISGLIYVWQIENPEVSYTYLPPKSPGINVDSYKRGHLSDSMKG 120
 DB 61 SCIDPHRHFMISGLIYVWQIENPEVSYTYLPPKSPGINVDSYKRGHLSDSMKG 120
 QY 121 FSLYKLVNTPDQTEGTCRVFMNTATELVKILEEVRILVAANSTPVISSDSNPGOE 180
 DB 121 FSLYKLVNTPDQTEGTCRVFMNTATELVKILEEVRILVAANSTPVISSDSNPGOE 180
 QY 181 RTYCMKSNKGPENLVWINTDMSLIDTALQNTVYLKLGIDYVSTRLPWTSGDY 240
 DB 181 RTYCMKSNKGPENLVWINTDMSLIDTALQNTVYLKLGIDYVSTRLPWTSGDY 240
 QY 241 LCCVENVALHQNITISQAESFTGNNTKNPQETHNELKVLVPLAVLAANAFTIYR 300
 DB 241 LCCVENVALHQNITISQAESFTGNNTKNPQETHNELKVLVPLAVLAANAFTIYR 300
 QY 301 RTPRHSTYGPVQLELTGHA 322
 DB 301 RTPRHSTYGPVQLELTGHA 322
 RESULT 2
 ICOL_HUMAN STANDARD; PRT; 302 AA.
 ID ICOL_HUMAN 075144; Q9NR01; Q9HD18;
 AC 075144; Q9NR01; Q9HD18;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
 DE (B7-related protein-1) (B7P-1)
 GN ICOSL OR B7H2 OR B7P1 OR KIAA0653.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Dendritic cell;
 RX MEDLINE=20477846; PubMed=11023515;
 RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
 RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds
 RT ICOS.";
 RL Blood 96:2808-2813(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC TISSUE=Peripheral blood lymphocytes;
 RX MEDLINE=20465019; PubMed=11007762;
 RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
 RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
 RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
 RT "Characterization of a new human B7-related protein: B7P-1 is the
 RT ligand to the co-stimulatory protein ICOS.";
 RL Int. Immunol. 12:1439-1447(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Leukocyte;
 RX MEDLINE=20126021; PubMed=10657606;
 RA Liong V., Wu P.W., Flinnerly H.F., Bean K.M., Spaulding V., Fouser L.A.,
 RA Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
 RA Jacobs K.A., Collins M.;
 RT "Identification of G150, a novel B7-like protein that functionally

RT binds to ICOS receptor.";
 RL J. Immunol. 164:1653-1657(2000).
 [4]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RA Ling V., Dunussi-Joannopoulos K.;
 RT "G150 molecules and uses therefor.";
 RL Patent number W00121796, 29-MAR-2001.
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
 CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
 CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,
 CC SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN
 CC LYMPH NODES, LEUKOCYTES AND SPLEEN.
 CC -1- INDICATION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
 CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
 CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- CAUTION: Ref.4 sequence differs from that shown in position 300
 CC onward for an unknown reason.
 CC
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 CC
 CC EMBL: AF199028; AAF34739.1; -;
 CC EMBL: AF289028; AAG01176.1; -;
 CC EMBL: AF216749; AAK16241.1; -;
 CC EMBL: AB014553; BAA31628.1; ALT-SEQ.
 CC EMBL: AX100595; CAC36465.1; -;
 CC MIM: 605717; -;
 CC InterPro: IPR003599; Iq.
 CC InterPro: IPR003006; Iq_MHC.
 CC InterPro: IPR003600; Iq_Like.
 CC Pfam: PF00047; Iq_3.
 CC SMART: SM00409; Iq; 1.
 CC SMART: SM00410; Ig_Like; 1.
 CC B-cell activation; Immune response; Glycoprotein;
 CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 CC Alternative splicing;
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 302 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 19 256 POTENTIAL.
 FT TRANSMEM 257 277 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 278 302 POTENTIAL.
 FT DOMAIN 30 120 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 151 223 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 37 113 POTENTIAL.

FT DISULFID 158 216 POTENTIAL.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 302 302 GHV -> ESNMLLLLS (IN ISOFORM 2).
 SQ SEQUENCE 302 AA; 33349 MW; 647934E21B5E34A CRC64;
 Query Match 35.5%; Score 599.5; DB 1; Length 302;
 Best Local Similarity 46.2%; Pred. No. 2,4e-41;
 Matches 140; Conservative 40; Mismatches 102; Indels 21; Gaps 8;
 QY 32 GLFLFLSSICAAETEGVAMGSSNVSLCIDPHRRHFLSLGLYYWQIENDEVSVTY 91
 DB 7 GLFLFLSSIRADQKEKVRAMVGSDELSCACPEGSRFLNDVYYWQESSEKTYVTH 66
 QY 92 LPYSPGINDSSKRNGLSLDSMKOGNSLYLKANTPDQDQEFRCRYMNTATLYKI 151
 DB 67 IPQSSLENDSSRYRNALMSPMGLMGDFSLRFNTPDQEQKFLCY-LSSLSGFQEV 125
 QY 152 LEEVRLRVAAVFSTPYISTDSSNPGO-ERYTCMSKNGPPEPNLYWINTDNLSDPA 210
 DB 126 LSEVTLHLVAANFVSVPVYSAFHS--PSQDELITFCISINGIPRPVYMIKTNLSLDOA 183
 QY 211 LQNTVYLLKGLYDVISTRLPMTSRGDVLCVENYALHQNTSISQASFTGN--- 266
 DB 184 LQNTVFLMNGGLDYVSVLRIARTPSVNIQCCIEVLLQONTLVGSG---TGNDIGER 239
 QY 267 ---TKNPQETNNEL---KVLVPLVLAANAAPVSTFYIKRTPRHRYTPKRY-QLEL 318
 DB 240 DKIEENPVSTGEKNAATWSILAVLCILVVAVALGWCRCRCLQH-SYAGAMAVSPETEL 298
 QY 319 TDH 321
 DB 299 TGH 301
 RESULT 3
 CD86_RABIT STANDARD; PRT; 330 AA.
 ID CD86_RABIT
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
 DE antigen).
 GN CD86.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHBB;HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules.";
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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RP • SEQUENCE FROM N.A.

Db 229 PW---SKPKQEPIDLPFWIIPVSGALVLTAVVLYCLACRHVARWKRTRRNEETVG 283

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OM protein - protein search, using sw model

```
Run on:      October 23, 2002, 13:25:56 ; Search time 24.8098 Seconds
              (without alignments)
              2245.253 Million cell updates/sec
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Title: US-09-728-420C-7
Perfect score: 1687
Sequence: 1 MQLKPCFVSLGTRQPVWK.....RPHRSYTPKTVQLTIDHA 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```

1:  sp.archaea:.*
2:  sp.bacteria:.*
3:  sp.fungi:.*
4:  sp.inuman:.*
5:  sp.invertebrate:.*
6:  sp.mammal:.*
7:  sp.mhc:.*
8:  sp.organelle:.*
9:  sp.phage:.*
10: sp.plant:.*
11: sp.podent:.*
12: sp.virus:.*
13: sp.vertebrate:.*
14: sp.unclassified:.*
15: sp.rvirus:.*
16: sp.bacteriap:.*
17: sp.archaeap:.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				ID	Description
No.	Score	Match	Length	DB		
1	365.5	21.7	296	13	062404	062404 gallus galli
2	246	14.6	316	4	09BXr1	09BXr1 homo sapien
3	181	10.7	329	6	09PTT2	09PTT2 canis famli
4	180	10.7	309	11	091Yv7	091Yv7 mus musculus
5	180	10.7	313	11	035531	035531 rattus norrv
6	178.5	10.6	356	11	064381	064381 mus musculus
7	175.5	10.4	323	6	09BDM9	09BDM9 macaca neme
8	175	10.4	314	11	061238	061238 mus musculus
9	175	10.4	325	5	002838	002838 mus scrofa
10	173.5	10.3	280	6	09GLJ3	09GLJ3 bos taurus
11	173	10.3	284	6	09PTT3	09PTT3 canis famli
12	172.5	10.2	323	6	09BDM4	09BDM4 macaca mula
13	172.5	10.2	329	6	09XSX6	09XSX6 felis silve
14	172.5	10.2	332	6	09GMZ7	09GMZ7 felis silve
15	172	10.2	332	6	095L16	095L16 felis silve
16	172	10.2	296	6	046405	046405 bos taurus

17	172	10.2	321	11	035187	Q35187	rattus norv
18	169.5	10.0	275	6	Q9BDN9	Q9BDN9	pepio anubi
19	169.5	10.0	323	6	Q9BDB8	Q9BDB8	cercocobus
20	169	10.0	292	6	Q9GMZ8	Q9GMZ8	fells alive
21	169	10.0	292	6	Q02758	Q02758	fells alive
22	167.5	9.9	323	6	Q9BDM2	Q9BDM2	cercophilthc
23	165	9.8	288	6	Q28439	Q28439	macaca mula
24	165	9.8	290	4	Q9NZ07	Q9NZ07	homo sapien
25	164	9.7	321	11	Q62524	Q62524	rattus norv
26	160	9.5	524	11	Q921K7	Q921K7	rattus norv
27	158.5	9.4	290	11	Q62680	Q62680	rattus norv
28	158	9.4	288	6	Q77684	Q77684	macaca neve
29	158	9.4	304	6	Q9T0X1	Q9T0X1	canis famil
30	155	9.2	321	11	Q55202	Q55202	rattus norv
31	151.5	9.0	526	4	Q9H458	Q9H458	homo sapien
32	150	8.9	149	11	Q62810	Q62810	rattus norv
33	148	8.8	288	6	Q9T770	Q9T770	sus scrofa
34	148	8.8	297	6	Q9BE99	Q9BE99	sus scrofa
35	147.5	8.7	306	11	Q9RJ29	Q9RJ29	mus muscula
36	147.5	8.7	584	4	Q00478	Q00478	homo sapien
37	146	8.7	288	6	Q9BDM6	Q9BDM6	cercocobus
38	146	8.7	289	6	Q28347	Q28347	cercocobus
39	144.5	8.6	235	6	Q9TQ58	Q9TQ58	canis famil
40	144.5	8.6	235	6	Q9N070	Q9N070	canis famil
41	142.5	8.4	290	11	Q9EP73	Q9EP73	mus muscula
42	142.5	8.4	319	4	Q00477	Q00477	homo sapien
43	142.5	8.4	334	4	Q9BUB1	Q9BUB1	homo sapien
44	142.5	8.4	357	4	Q15338	Q15338	homo sapien
45	142.5	8.4	359	4	P78410	P78410	homo sapien

	RESULT	1	
042404	ID	PRELIMINARY:	PRT: 296 AA.
AC	042404;		
DT	01-JAN-1998 (Tremblrel, 05, Created)		
DT	01-JAN-1998 (Tremblrel, 05, Last sequence update)		
DT	01-DEC-2001 (Tremblrel, 19, Last annotation update)		
DE	CBB0-LIKE PROTEIN.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauilia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCHI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=WHITE LEGHORN;		
RC	O'Regan M.N.;		
RT	"Chicken CD28 ligands."		
RL	Submitted (OCT-1996) to the EMBL/genbank/DBDJ databases.		
DR	EMBL, Y08823; CAA70058.1; -.		
DR	InterPro: IPR003599; Ig.		
DR	InterPro: IPR003600; Ig_Like.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	Pfam: PF00047; Ig_2.		
DR	SMART: SMO0409; IG_1.		
DR	SMART: SMO0410; IG_Like; 1.		
SQ	SEQUENCE 296 AA; 3315 MW; 061572FEB238C76 CRC64;		
	Query Match	21.7%; Score 365.5; DB 13; Length 296;	
	Best Local Similarity	35.6%; Pred. No. 1,7e-23;	
	Matches 106; Conservative 47; Mismatches 122; Indels 23; Gaps		10
QY	30 GLGLLELLLSLCAASAEFEVCGAMGGSNYVLSCIDPHRRHRNLISGLVYWQIENPE---85 : : : : : Db 5 GYGFLLEHLFIHLRAVATALEKRIISKPDNNATLSCIYAN-RGFDDLSLRWYQIDGVESKS 63		
OY	86 VSVYYLYLPYSPGIWD-SKYNRGHSLSDSKSGNESLYLKNTVPDQTDFTCRYVMNT 144 : : : : : : Db 64 CSVAHALISGDNDSEOGCSGFKNRQLMDKRGDDDFSLILYNROSDEHYKC-VYMOT 122		

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QY 145 ATELVLILEEVRRLRYAANFSTPVIS--TSDSSNPGOERTYTCMSKNGYPEPNLYWINT 202
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 123 IEXTVLIHQEQVYLSLAASQPIISGPIRNSYTGCEVTFGCRSDNGSPERNVYWINT 182
QY 203 DNSLITFALQNNVTYLNKGLDYVISTLRPMTSRGDVLCVEENVALHONITSISOESF 262
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 183 DNRRLSOSPFNITQHPD--GTYSVLSTLKVNATSDMCEFTENKVLQEN--TSANYTEEM 239
QY 263 TGNNTKNPOETHNNELK-----VLVPVLAALAAAFVSFLI---YRRRPHRSTGP 311
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 240 QNNGSST--GSHKDAKGGOGAQAANVSVILMAFLVLICMLWRRSFQLVSTAP 295

RESULT 2
Q9BXRL PRELIMINARY: PRT: 316 AA.
AC Q9BXRL;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
01-JUN-2001 (TREMBlrel. 17, Last sequence update)
01-DEC-2001 (TREMBlrel. 19, Last annotation update)
COSTIMULATORY MOLECULE.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=21163383; PubMed=11224528;
RA Chapoval A.I., Ni J., Lau J.S., Wilcox R.A., Flies D.B., Liu D.,
RA Dong H., Sica G.L., Zhu G., Tamada K., Chen L.,
RT "B7-H3: A costimulatory molecule for T cell activation and IFN-gamma
RT production."
RT Nat. Immun. 2:269-274(2001).
RL EMBL: AF302102; AAK15438.1;
DR InterPro: IPR003598; I9_
DR InterPro: IPR003598; I9_G2.
DR InterPro: IPR003600; I9_Like.
DR InterPro: IPR003606; I9_MHC.
DR Pfam: PF00047; I9_2.
DR SMART: SM00409; I9_2.
DR SMART: SM00408; I9_G2; 2.
DR SMART: SM00410; I9_Like; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 316 AA; 33791 MW; FP97007F191CCFA1 CRC64;

Query Match 14.6%; Score 246; DB 4; Length 316;
Best Local Similarity 30.6%; Pred. No. 3.6e-13;
Matches 86; Conservative 42; Mismatches 123; Indels 30; Gaps 8;

QY 21 LHVSGGFPSGLG-LFLLLSLCAASAEETEGAVGNSVNLSCIDPHRRHFNLSGLVYVW 79
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 12 VHVG---AALGALMECLTGALLEVQVPEDPVVALVGTDTLCCSPSPERGSLAQLNLIM 67
QY 80 QIENPEVSTYVLYPKSPININDSSKNGHLSIDSMOGNSLYLKAVTPQDTQEFIC- 138
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 68 QLTDTKQLVHSF---AEQDDGSAVANTALFPLLLAOGNASLRLQRRVADEGSFTCF 123
QY 139 ---RVFMNATATELVILEEVRRLRYAANFSTPVISTDSSN--POEERTYTCMSKNGYPE 193
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 VSTRDGSAA-----VSLQVAAPYSKRSMLEPRKDLRPDPTYTITCSSRGTPE 173
QY 194 PNLVWINTTNSLIDTALQNNVTYLNKGLDYVISTLRPMTSRGDVLCVEENVALHONI 253
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 174 AEVFMQDGGVPL--TGAVTTTSMANEOGLFDVHSVLRVLCANGTYSCLVNPVLAQDA 231
QY 254 TTSQAESTFTGNNTKNPOETHNNELKVLVPVLAALAAAFV 294
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 232 HG---SVTITGQPMTFPEPALMVTVGLSVCLIALVLAFAV 269

RESULT 3
Q9TTP2
```

```
ID Q9TTP2 PRELIMINARY: PRT: 329 AA.
AC Q9TTP2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE B7-2 PROTEIN.
GN CD86.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9613;
RN [1]
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT Molecules."
RL Immunogenetics 50:349-353(1999).
DR EMBL: AF106826; AAF17297.1;
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003596; I9_V.
DR SMART: SM00406; I9_1.
DR PROSITE: PS00290; I9_MHC; UNKNOWN_1.
SQ SEQUENCE 329 AA; 37774 MW; D98BB63437BF7B73 CRC64;

Query Match 10.7%; Score 181; DB 6; Length 329;
Best Local Similarity 26.1%; Pred. No. 1.5e-07;
Matches 78; Conservative 46; Mismatches 123; Indels 52; Gaps 13;

QY 33 LFLLLSLCAASAEETEGAVGNSVNLSCIDPHRRHFNLSGLVYVQIENPEVSTYVYL 92
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 13 LFVMTLLLYGAASMSQ--AFVFKTGELPCHFTNSQNISDELVEVFODDKLVLVELYR 70
QY 93 PYKSPGINVDSYKRNHGLSIDSMOGNSLYLKAVTPQDTQEFICVFNMTATELVYL 152
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 71 GKENPQ--NVRKKYGR-----TSPDKDNTLRNLHIDIKKGLQCFVHHKGRKGLVPMH 124
QY 153 EEVRLRYAANFSTP-VISTDSSNPGOERTYTCMSKNGYEP-NLYWINTTNS--LLID 208
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 125 QMSNDLSYANFSQPELMTVNSNRTEGSLINLCSSIQGVPEPKEMFLVKTENSSPKVD 184
QY 209 TAL---QNNVYLNKGLDYVISTLRPMTSRGDVLCVE-----NVALHON 252
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 185 TVMKRSQNNVT---ELYNVISLSFSVPEASVNSIFCVLQDESMKPLSPYINDAHTR 239
QY 253 TTSISOAESFTGNNTKNPOETHNNELKVLVPVLAALAAAFVSFLIYRRPHRSTGP 311
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 240 PT-----PDGDHILMIALLVMLVILCGVVF--FLTRKRK--KKQPGP 279

RESULT 4
Q91YV7 PRELIMINARY: PRT: 309 AA.
AC Q91YV7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CD86 ANTIGEN.
OS Mus musculus (Mouse).
OC Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=20093996; PubMed=10630300;
RA Strassberg R.;
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013807; AHI13807.1;
SQ SEQUENCE 309 AA; 34714 MW; 61593C49EFCB0CE5 CRC64;

Query Match 10.7%; Score 180; DB 11; Length 309;
Best Local Similarity 23.8%; Pred. No. 1.7e-07;
Matches 64; Conservative 53; Mismatches 128; Indels 24; Gaps 8;
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:27:51 ; Search time 14.6361 Seconds
(without alignments)
1890.790 Million cell updates/sec

Title: US-09-728-420C-12

Perfect score: 1495

Sequence: 1 MRLSPGLLFLLFSSLRADT.....VAVAGWVCRDCLQHSYAG 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

T number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194.5	13.0	487	2 S65133	butyrophillin - mou
2	182	12.2	309	2 I49522	gene B7-2 protein
3	179	12.0	526	2 S70587	butyrophillin precu
4	171.5	11.5	275	2 JC7604	CD86 spliced varia
5	171	11.4	526	2 A37821	butyrophillin - bov
6	165.5	11.1	329	1 A48754	B7-2 antigen - hum
7	164.5	11.0	288	2 A45803	B-cell-restricted
8	158	10.6	330	2 I46691	CD86 precursor - r
9	145.5	9.5	289	2 G00031	B-lymphocyte activ
10	142.5	9.5	289	2 G00031	B7 protein - red-c
11	140.5	9.4	321	2 T54766	B-lymphocyte activ
12	139	9.3	274	2 A47639	OX-2 membrane glyco
13	135	9.0	299	2 I46690	CD80 precursor - r
14	133.5	8.9	509	2 JC5288	SHP substrate-1 pr
15	133.5	8.9	513	2 JC5289	SHP substrate-1 pr
16	124	8.3	278	1 TDRTOX	OX-2 membrane glyco
17	123	8.2	333	2 A31923	amalgam protein pr
18	122	8.2	646	2 I38049	cell surface glyco
19	117.5	7.9	946	1 A47299	cor-related recept
20	115.5	7.7	1256	2 T03096	CD0 protein - rat
21	115	7.7	739	2 A41288	vascular cell adhe
22	114	7.6	647	2 B41288	vascular cell adhe
23	114	7.6	662	2 T16525	hypothetical prote
24	114	7.6	702	2 A36319	carcinoembryonic a
25	112	7.5	503	2 JC5287	SHP substrate-1 pr
26	111.5	7.5	569	2 A46462	T cell activation
27	110	7.4	299	2 S56749	functional adhesio
28	109.5	7.3	978	2 S16385	macrophage colony-
29	108.5	7.3	1896	2 T08851	down syndrome cell

30	107	7.2	234	2 S14237	Ig kappa chain pre
31	107	7.2	1087	2 I51552	platelet-derived g
32	107	7.2	1098	1 PFM5RB	platelet-derived g
33	106	7.1	584	2 I50419	s-glycerin precuro
34	105.5	7.1	477	1 I73631	brain-derived neur
35	105.5	7.1	822	1 A56853	brain-derived neur
36	105	7.0	588	2 JH0506	adhesion molecule
37	105	7.0	588	2 A45254	surfacte glycoprote
38	104.5	7.0	246	2 A47712	myelin/Oligodendro
39	104	7.0	1051	2 A39712	kinase-like protei
40	103.5	6.9	976	1 TVMSMD	macrophage colony-
41	103	6.9	538	2 JC2457	vascular cell adhe
42	103	6.9	739	2 JN0581	vascular cell adhe
43	102.5	6.9	1880	2 T18531	tractin - medica
44	102	6.8	351	2 S39603	class I histocompa
45	101.5	6.8	1091	2 A58532	glial cell membran

ALIGNMENTS

RESULT 1

S65133

butyrophillin - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999

C:Accession: S65133

Rishili, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.

Biochim. Biophys. Acta 1245, 285-292, 1995

A:Title: Carboxy-terminal cytoplasmic domain of mouse butyrophillin specifically assoc

A:Reference number: S65133; MUID:96125722

A:Accession: S65133

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-487 <ISH>

A:Cross-references: GB:580642; NID:g1246078; PIDN:AAB35893.1; PID:g1246079

Query Match

Best Local Similarity 13.0%; Score 194.5; DB 2; Length 487;

Matches 65; Conservative 35; Mismatches 93; Indels 13; Gaps 9;

QY	25	VRAWVS-DVELSCACPPGSRFLNDYVYWMQTSKTVYVYH:PNSSLENNVDSRRNR 83
DB	1	VLAIVGSDDAELTCGFSPNASSETWELMFRQT-RSTAVLLYRPGQEGQQM-TEYRGR 58
QY	84	ALMSFAGMLRGDFSLRLFNVPPODEKFCVLTSOSLGFQELVSEVTLVHVAANFSVPV 143
DB	59	ATLAAGLLDGRATLLIRVDFSDQGEYRCL-FKNDNDFEE--AAVYLKVAAGSDPOI 114
QY	144	SAPHSODELTFCTGTSINGYPRPNVYVINKTDN-SLIDQALQNDYVFLNMRGLDYVSV 202
DB	115	SWT-VOENGEMELECTSSGWYPEPOVW-RTGNREMLPST--SDSKKHNEGLETVAVS 169
QY	203	LRIARTPSVNIQCIEENLLOONLTV 228
DB	170	MMISDSIKMNSCCIQNTLLGQKEV 195

RESULT 2

I49522

gene B7-2 protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I49522

R.Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim

J. Exp. Med. 178, 2185-2192, 1993

A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell

A:Reference number: I49522; MUID:94065585

A:Accession: I49522

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-309 <RES>

A:Cross-references: GB:I25606; NID:g432478; PIDN:AAA79770.1; PID:g432479

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:23:41 ; Search time 8.49836 Seconds
(without alignments)
1312.163 Million cell updates/sec

Title: US-09-728-420c-12
Perfect score: 1495
Sequence: 1 MRLGSPGLFLFLFSSLRADT.....VAVALGWCRDRCLOHSTAG 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
T number of hits satisfying chosen parameters: 105224
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1495	100.0	302	1	ICOL_HUMAN 075144 homo sapien
2	588.5	39.4	322	1	ICOL_MOUSE Q93H18 mus musculu
3	203	13.6	524	1	BURY_MOUSE O62556 mus musculu
4	182	12.2	309	1	CD86_MOUSE P42082 mus musculu
5	179	12.0	526	1	BURY_MOUSE Q13410 homo sapien
6	167	11.2	526	1	BURY_BOVIN P18892 bos taurus
7	165.5	11.1	329	1	CD86_HUMAN P42081 homo sapien
8	164.5	11.0	288	1	CD80_HUMAN P33681 homo sapien
9	158	10.6	330	1	CD86_RABIT P42071 oryctolagus
10	151.5	10.1	306	1	CD80_MOUSE Q00609 mus musculu
11	139	9.3	274	1	OX2G_HUMAN P41217 homo sapien
12	135	9.0	299	1	CD80_RABIT P42070 oryctolagus
13	144	8.3	278	1	OX2G_RAT P04218 rattus norv
14	123	8.2	298	1	P57087 homo sapien
15	123	8.2	333	1	AMAL_DROME P15364 drosophila
16	122	8.2	646	1	MU18_HUMAN P43121 homo sapien
17	115	7.7	739	1	VCA1_HUMAN P19320 homo sapien
18	114	7.6	702	1	CEA5_HUMAN P06731 homo sapien
19	111.5	7.5	569	1	TACT_HUMAN P40200 homo sapien
20	110	7.4	299	1	JAM1_HUMAN O9y624 homo sapien
21	109.5	7.3	978	1	KFMS_RAT O00495 rattus norv
22	108.5	7.3	2012	1	DSCA_HUMAN O60469 homo sapien
23	107	7.2	1087	1	PCDS_XENLA P26619 xenopus lae
24	107	7.2	1098	1	PGOR_MOUSE P05622 mus musculu
25	105.5	7.1	300	1	JAM1_MOUSE O88792 mus musculu
26	105.5	7.1	822	1	TRKB_HUMAN O16620 homo sapien
27	105	7.0	588	1	C166_CHICK P42292 gallus gall
28	104.5	7.0	246	1	MOS_BOVIN P55803 bos taurus
29	104	7.0	976	1	KFMS_MOUSE P05581 mus musculu
30	104	7.0	1051	1	PTK7_CHICK Q91048 gallus gall
31	103	6.9	739	1	VCA1_MOUSE P29533 mus musculu
32	100.5	6.7	517	1	PVRL_HUMAN Q15223 homo sapien
33	99.5	6.7	583	1	C166_MOUSE Q61490 mus musculu

ALIGNMENTS

RESULT 1	ICOL_HUMAN	STANDARD:	PRT:	302 AA.	O16653 homo sapien
ID	ICOL_HUMAN	075144; Q9NRQ1; Q9HD18;			O63345 rattus norv
AC	15-JUL-1999 (Rel. 38, Created)				P32507 mus musculu
DT	16-OCT-2001 (Rel. 40, Last sequence update)				P16621 drosophila
DR	01-MAR-2002 (Rel. 41, Last annotation update)				O9x156 bos taurus
DE	ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein GL150)				001965 mus musculu
DE	(B7-related protein-1) (B7RP-1).				008180 drosophila
GN	ICOSL OR B7H2 OR B7RP1 OR KIAA0653.				O26474 schistocerc
OS	Homo sapiens (Human).				O9x176 sus scrofa
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				013308 homo sapien
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				O61885 mus musculu
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Dendritic cell;				
RX	MEDLINE=20477846; PubMed=11023515;				
RA	Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;				
RT	"Costimulation of T cells by B7-H2, a B7-like molecule that binds				
RT	ICOS."				
RL	Blood 96:2808-2813(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.				
RC	TISSUE=Peripheral blood lymphocytes;				
RX	MEDLINE=20465019; PubMed=11007762;				
RA	Yoshinaga S.K., Zhang M., Piscillo J., Horan T., Khare S.D., Miner K.,				
RA	Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,				
RA	Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;				
RT	"Characterization of a new human B7-related protein: B7RP-1 is the				
RT	ligand to the co-stimulatory protein ICOS."				
RL	Int. Immunol. 12:1439-1447(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RC	TISSUE=Leukocyte;				
RX	MEDLINE=20126021; PubMed=10657606;				
RA	Ling V., Wu P.W., Finererty H.F., Bean K.M., Spaulding V., Fouser L.A.,				
RA	Leonard J.P., Hunter S.E., Zoliner R., Thomas J.L., Miyashiro J.S.,				
RA	Jacobs K.A., Collins M.;				
RT	"Identification of GL50, a novel B7-1-like protein that functionally				
RT	binds to ICOS receptor."				
RL	J. Immunol. 164:1653-1657(2000).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=98403880; PubMed=9734811;				
RA	Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,				
RA	Kotani H., Nomura N., Ohara O.;				
RT	"Prediction of the coding sequences of unidentified human genes. X.				
RT	The complete sequences of 100 new cDNA clones from brain which can				
RT	code for large proteins in vitro."				
RL	DNA Res. 5:169-176(1998).				
RN	[5]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RC	Ling V., Dunussi-Joannopoulos K.;				
RT	"GL50 molecules and uses therefor."				

```

RL Patent number W00121796, 29-MAR-2001.
CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein (By similarity).
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUCOCYTES,
CC SPLEEN, THYMUS AND TONSIL). WHILE ISOFORM 2 IS DETECTED ONLY IN
CC LYMPH NODES, LEUCOCYTES AND SPLEEN.
CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. B7N/MOG
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- CAUTION: Ref.4 sequence differs from that shown in position 300
CC onward for an unknown reason.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF199028; AAF34739.1; -
DR EMBL: AF289028; AAG01176.1; -
DR EMBL: AF216749; AAK16241.1; -
DR EMBL: AB014553; BAA31628.1; ALT_SEQ.
DR EMBL: AX100595; CAC36465.1; -
DR MIM: 605717; -
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00409; Ig_1.
DR SMART: SM00410; Ig_Like_1.
KW B-cell activation; Immune response; Glycoprotein;
KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;
KW Alternative splicing.
FT CHAIN 1 18 POTENTIAL.
FT DOMAIN 19 302 ICOS LIGAND.
FT TRANSMEM 257 277 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 278 302 POTENTIAL.
FT DOMAIN 30 120 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 151 223 IG-LIKE V-TYPE DOMAIN.
FT DISULFID 37 113 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 158 216 POTENTIAL.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 300 302 GHV -> ESMNILLIS (IN ISOFORM 2).
SQ SEQUENCE 302 AA; 33349 MW; 647934E21B53E34A CRC64;

Query Match 100.0%; Score 1495; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 1,4e-122;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSGPGLFLFLSSLRADTQERKVRAMGSDVELSCACPEGRSFDLNDVYVWQTSSEK 60
DB 1 MRGSGPGLFLFLSSLRADTQERKVRAMGSDVELSCACPEGRSFDLNDVYVWQTSSEK 60


```

RA Ling V., Dunussi-Joannopoulos K.:
 RT "G150 molecules and uses therefor."
 RL Patent number WO0121796, 29-MAR-2001.
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION. INDICES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
 CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
 CC TH2 PHENOTYPE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
 CC (PARTICULARLY IN THE CORTX AND IN BOTH PRIMARY AND SECONDARY
 CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PETER'S
 CC PATCHES (MOSTLY IN THE FOLLICLES). LOWER LEVELS IN MANY
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
 CC CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
 CC -1- DEVELOPMENTAL STAGE: DETECTED EARLY IN EMBRYONIC STAGE. IN THE YOLK
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
 CC 14.5 DPC.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF216747; AAF45149.1; -
 DR EMBL: AP199027; AAF34738.1; -
 DR EMBL: AX100591; CAC36463.1; -
 DR EMBL: AX100593; CAC36464.1; -
 DR EMBL: AE394451; AAK77544.1; -
 DR MGD: MGI:1354701; Icosl.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00410; Ig_Like; 1.
 KW B-cell activation. Immune response. Glycoprotein;
 KW Immunoglobulin domain. Signal. Transmembrane; Multigene family;
 KW Alternative splicing.
 FT SIGNAL 46
 FT CHAIN 1
 FT CHAIN 47 322
 FT DOMAIN 277 298
 FT TRANSEM 298 298
 FT DOMAIN 299 322
 FT DOMAIN 55 145
 FT DOMAIN 178 250
 FT DOMAIN 31 38
 FT DOMAIN 289 292
 FT DISULFID 62 138
 FT DISULFID 185 243
 FT CARBOHYD 71 71
 FT CARBOHYD 120 120
 FT CARBOHYD 163 163
 FT CARBOHYD 200 200
 FT CARBOHYD 213 213
 FT CARBOHYD 252 252
 FT CARBOHYD 265 265

FT VARSPIC 321 322 HA -> TWAPVPODYIIPRYLMSPLCKTRGLP (IN
 FT CONFLICT 237 237 ISOFORM 2).
 FT SEQUENCE 322 AA; 35960 MW; 55CBAAD12E47E6 CRC64;
 SQ
 Query Match 39.4%; Score 588.5; DB 1; Length 322;
 Best Local Similarity 46.6%; Pred. No. 7.7e-44;
 Matches 135; Conservative 39; Mismatches 97; Indels 19; Gaps 7;
 QY 7 GLPLFLPSLADYOEKVRAMVGSDELSCACPEGSFRLDNDVYVYQTSSEKTVYTH 66
 DB 32 GLPLFLSLSCAASETELVGAMGSNNVLSCLDPHRRFNLSGLYVWQLENEPEVSTY 91
 QY 67 IPONSLENDRTNRRLMSBAGMLKDESLRFPNTPODEQFRLYVLSQSLGQEV 125
 DB 92 LPKSPGAINVSSYKRNCHLSIDSMKQGNFSLYLNKNTPODQETGVRVKNATPELKI 151
 QY 126 LSEVETLVAAAFSPVAVSAPHS--PSODELFTCTCSINGPRPNVYINKTDSLDOA 183
 DB 152 LEEVRLRVAANFSTPVLSTSDSSNPGO-ERTYCMKSNKGIPEPNLINTTDSLIDTA 210
 QY 184 LQNDTVFLMRLGIDVSVLRARTPSVNICCIENVLLONTLVGSG--TGNDIGER 239
 DB 211 LQNTTVLNLKGLVYISTRLPWTSGDVLQVENVALLHQNTISQAESFTGNN---- 266
 QY 240 DKITENPVSTGEKNAATWSILAVALCLVVAVALGWCRCLOH-STAG 288
 DB 267 ---TKNPQETHNNEL---KVLVPLVLAALAAAFVSFIYRTRRPHRSYTG 310
 RESULT 3
 BUTY_MOUSE STANDARD; PRT; 524 AA.
 AC BUTY_MOUSE Q62556; P97392;
 ID 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Butyrophillin precursor (BT).
 GN BTNL1 OR BTN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary gland;
 RX MEDLINE=97148936; PubMed=8995761;
 RA Ogg S.L., Komaragiri M.V.S., Mather I.H.;
 RT "Structural organization and mammary-specific expression of the
 RT butyrophillin gene".
 RL Mam. Genome 7:900-905(1996).
 RN [2]
 RP SEQUENCE OF 39-487 FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=96125722; PubMed=8541302;
 RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;
 RT "Carboxy-terminal cytoplasmic domain of mouse butyrophillin
 RT specifically associates with a 150-kDa protein of mammary epithelial
 RT cells and milk fat globule membrane".
 RL Biochim. Biophys. Acta 1245:285-292(1995).
 CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
 CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
 CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
 CC MEMBRANE (BY SIMILARITY).
 CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
 CC ASSOCIATION WITH THE MILK-FAT GLOBULE MEMBRANE DURING LACTATION.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF
 CC PREGNANCY AND IS MAXIMAL DURING LACTATION.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_Taxid=10090;
CC	[1]
CC	SEQUENCE FROM N.A.
RX	MEDLINE=94065585; PubMed=7504059;
RA	Freeman G.J., Borriello F., Hodes R.J., Retser H., Gitben J.G.,
RA	Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,
RA	Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
RT	"Murine B7-2, an alternative CTL4 counter-receptor that costimulates
RT	T cell proliferation and interleukin 2 production.";
RL	J. Exp. Med. 178:2185-2192(1993).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129;
RX	MEDLINE=96094437; PubMed=7499829;
RA	Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT	"Differential expression of alternate mb7-2 transcripts.";
RL	J. Immunol. 155:5490-5497(1995).
RN	[3]
RP	SEQUENCE OF 7-309 FROM N.A.
RX	MEDLINE=94230971; PubMed=7513726;
RA	Chen C., Gault A., Shen L., Nabavi N.;
RT	"Molecular cloning and expression of early T cell costimulatory
RT	molecule-1 and its characterization as B7-2 molecule.";
RL	J. Immunol. 152:4929-4936(1994).
CC	-1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC	FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC	BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC	EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NATIVE T CELLS,
CC	SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
CC	CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
CC	-----
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CC	-----
DR	EMBL; L25606; AAA79770.1; -
DR	EMBL; U39456; AAC52334.1; -
DR	EMBL; U39459; AAC52334.1; JOINED.
DR	EMBL; U39461; AAC52334.1; JOINED.
DR	EMBL; U39462; AAC52334.1; JOINED.
DR	EMBL; U39463; AAC52334.1; JOINED.
DR	EMBL; U39464; AAC52334.1; JOINED.
DR	EMBL; U39465; AAC52334.1; JOINED.
DR	EMBL; U39466; AAC52334.1; JOINED.
DR	EMBL; U39456; AAC52336.1; JOINED.
DR	EMBL; U39461; AAC52336.1; JOINED.
DR	EMBL; U39462; AAC52336.1; JOINED.
DR	EMBL; U39463; AAC52336.1; JOINED.
DR	EMBL; U39464; AAC52336.1; JOINED.
DR	EMBL; U39465; AAC52336.1; JOINED.
DR	EMBL; U39466; AAC52336.1; JOINED.
DR	EMBL; S70108; AAB30744.2; ALT_INIT.
DR	MGD; MGI:101773; Cd86.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	SMART; SM00406; IGY; 1.
DR	PROSITE; PS00290; IG_MHC; FALSE_NEG.
DR	Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
DR	Receptor.
DR	-----
CC	CHAIN 1 23 POTENTIAL.
CC	-----
CC	T LYMPHOCYTE ACTIVATION ANTIGEN CD86
CC	-----

QY 117 SQSLSGFEVLVSVE-VTLHVAANFSPVVASPHSPSQ---DELFTCTGTSINGYPRPNVWT 172
 121 -QTETRYRVLHQEQVVLASVLAASYSQPILSGPIRNSYSTGEVYFSCRSNDGYPEPNVWT 179
 QY 173 NKTNSLLDQALQNDYFLNMKRGILDYVSVLRARLPSPVNICCIENVLQONLTV---- 228
 180 NRIDNTFLSSQDFNIT--QHPRDGYSVLSTLKVNATSDMOLECFIEKNVLOENTSANYTE 237
 QY 229 ----GSQTNDIGERDKITENPSTGEKNATWSILAVCLIVVAVAIAGWCRCRCIQ 283
 238 EMQNGSSSTG-----SHKDAKKGCGCAQAANAAYSVILMAFLTVLCLWMRRRSFQ 288

RESULT 2
 ID Q9BXRL PRELIMINARY; PRT; 316 AA.
 AC Q9BXRL;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 01-JUN-2001 (TReMBLrel. 17, last sequence update)
 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 COSTIMULATORY MOLECULE.
 Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21163383; PubMed-11224528;
 RA Chappoval A.I., Ni J., Lau J.S., Micox R.A., Files D.B., Liu D.,
 Dong H., Sica G.L., Zhu G., Tamada K., Chen L.,
 RT "b7-h3: A costimulatory molecule for T cell activation and IFN-gamma
 production.";
 RT Nat. Immun. 2:269-274(2001).
 RL EMBL: AF302102; AAK15438.1;
 DR InterPro: IPR003599; Ig_
 DR InterPro: IPR003598; Ig_C2
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: SM00410; IG_Like; 2.
 DR Immunoglobulin domain.
 SQ SEQUENCE 316 AA; 33791 MW; FF97007F191CCFAL CRC64;

Query Match 19.7%; Score 294.5; DB 4; Length 316;
 Best Local Similarity 31.1%; Pred. No. 3.6e-20;
 Matches 93; Conservative 40; Mismatches 111; Indels 55; Gaps 11;

QY 2 RLGSFG-----LFLFLSSLRADTQKEKVRAMVGSDELSCACPEGSFRDLNDV 50
 4 RRGSPGAGVHGAALGALWFCILGALVEQVPEDPVALVGTDATLCCSPSPGFSIAQL 63
 DB 4 RRGSPGAGVHGAALGALWFCILGALVEQVPEDPVALVGTDATLCCSPSPGFSIAQL 63
 QY 51 YVWMTSEKTVYTHIQNSSLEND--SRYRNRALMSRPAQLRQDFSLRFENYTPODE 108
 64 NLWMLQTLDRQLV-----HSFAEGDQGSAAVNRALRFPDLAQGNALRLQORVAD 117
 QY 109 QKFHCLVLSLGFQEVLSVEVTLHVAANFSPVVASPHSPSQ---DELFTCTGTSING 163
 118 GSTCTCVSIRDFG-----SAASVLOVAARYSKP--SMTLEPKDKLRPGGVITITSSYRG 170
 DB 164 YPRPNVYW-----INKTNSLLDQALQNDYFLNMKRGILDYVSVLRARLPSPVNICCIE 218
 171 YPEAEVFWMDGGQVPLTGVNITSQ-----MANEQGLFDVSHVLRVYLGANGTYSCLVR 223
 QY 219 NVTLQONLTVGSGTNDIGERDKITENPSTGEKNATWSILAVCLIVVAVAIAGWC 277
 DB 224 NPVLQOD-AHGSVT-----ITGQPMTPPPE--ALWVTGLSVCLIALLVALAFVC 270

RESULT 3
 Q921K7

ID Q921K7 PRELIMINARY; PRT; 524 AA.
 AC Q921K7;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE SIMILAR TO BOTRYOPHILIN, SUBFAMILY 1, MEMBER A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011497; AAH11497.1;
 SQ SEQUENCE 524 AA; 58433 MW; 6BDFEBC6E191E224 CRC64;

Query Match 14.0%; Score 209; DB 11; Length 524;
 Best Local Similarity 31.2%; Pred. No. 1.3e-11;
 Matches 65; Conservative 37; Mismatches 94; Indels 12; Gaps 8;
 QY 22 EKEVRAMVGSDELSCACPEGSFRDLNDVYVYVMTSEKTVYTHIQNSSLENDVSRIR 81
 DB 36 QEPVALVGSDAELTQGFSPNASSRYMELMFROT-RSKAVLLYRDQOEGQOM-TEYR 93
 QY 82 NRALSPAGMLRGDFSLRFLFNVTPODEQKHFHCLVLSLGFQEVLSVEVTLHVAANFSPV 141
 DB 94 GRATLATATGLDGRATTLIRVYRSDGEYRCL-FKNDDEE--AAVYLKAAVASSDP 149
 QY 142 VVSAPHSSQDELFTCTGTSINGYPRPNVWINKTDN-SLDQALQNDYFLNMKRGILDYV 200
 DB 150 QISMT-VOENGEEMLECTSSGMYPEPQYQW--RTGNREMLPST--SESKHNEGLFTVA 204
 QY 201 SVLRARLPSPVNICCIENVLQONLTV 228
 DB 205 VSMNRDSSINMSSCIONILLGQKEY 232

RESULT 4
 ID Q9BDM2 PRELIMINARY; PRT; 323 AA.
 AC Q9BDM2;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE CD86 PROTEIN.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OC NCBI_TaxId=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21383618; PubMed-11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-Ligand and co-stimulatory molecules.";
 RT J. Immunogenetics 53:315-328(2001).
 RL EMBL: AF344661; AAK37543.1;
 DR InterPro: IPR003599; Ig_
 DR InterPro: IPR003596; Ig_V.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 SQ SEQUENCE 323 AA; 37045 MW; 3E43152A8FD17267 CRC64;

Query Match 12.4%; Score 185; DB 6; Length 323;
 Best Local Similarity 23.2%; Pred. No. 1.4e-09;
 Matches 68; Conservative 59; Mismatches 120; Indels 46; Gaps 13;
 QY 7 GLFLFLF--SSLRADTQKEKVRAMVGSDELSCACPEGSFRDLNDVYVYVMTSEKTVY 64
 DB 2 GLINILFVMAFLISGAAPLKIQAVENETADLPQAFANSONRSSELVYFWQNDENLYLNE 61

GenCore version 5.1.3
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OM protein - protein search, using sw model

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Run on:      October 23, 2002, 13:16:41 ; Search time 25.9672 Seconds
              (without alignments)
              1231.909 Million cell updates/sec
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Title: US-09-728-420C-12

Sequence: 1 MRLGSPGLFLFLSSLRADT.....VAVAIGWVCRRDCLQHSYAG 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

Database : A.GeneSeq.032802.*

1:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1987.DAT.*
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11:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1991.DAT.*
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15:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1995.DAT.*
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18:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/geneSeq/geneSeqp-emb1/AA2001.DAT.*

SUMMARIES

Result	No.	Score	Query		Length	DB	ID	Description
			Match					
1	1495	100.0	288	21	AAB08727	Amino acid sequenc		
2	1495	100.0	302	21	AAB08729	Amino acid sequenc		
3	1495	100.0	302	22	AAG67292	Amino acid sequenc		
4	1495	100.0	309	22	AAB67713	Amino acid sequenc		
5	1495	100.0	516	22	AAU00422	Human B7-3 protein		
6	1494	99.9	343	22	ABBI0322	Human cDNA SEQ ID		
7	1494	99.9	345	22	ABBI0652	Human cDNA SEQ ID		
8	1494	99.9	345	22	AAU18065	Human immunoglobulin		
9	1494	99.9	370	22	AAU18005	Human immunoglobulin		
10	1490	99.7	302	22	AAB87395	Human gene 2 encod		
11	1490	99.7	344	22	ABBI0504	Human cDNA SEQ ID		

12	1490	99.7	344	22	AAU18067	Human immunoglobulin
13	1236	82.7	239	22	AAU00423	Human B7-3 soluble
14	1218	81.5	490	22	AAAB67718	Amino acid sequenc
15	588.5	39.4	322	21	AAAB08725	Amino acid sequenc
16	588.5	39.4	322	22	AAAB67711	Amino acid sequenc
17	588.5	39.4	347	22	AAAB67712	Amino acid sequenc
18	577	38.6	133	22	AAAB67715	Protein encoded by
19	559.5	37.4	489	22	AAAB67719	Amino acid sequenc
20	539	36.1	329	21	AAAB08730	Amino acid sequenc
21	490.5	32.8	280	21	AAAB08728	Amino acid sequenc
22	290.5	19.4	316	20	AAV41705	Human PRO352 protea
23	290.5	19.4	316	21	AAAB44261	Human PRO352 (UNC3
24	290.5	19.4	316	22	AAU290505	Human PRO polypept
25	290.5	19.4	316	22	AAU008946	Human B7-H3 polype
26	290.5	19.4	316	22	AAAB87394	Human gene 2 encod
27	273.5	18.3	534	22	AAAB00906	Human B lymphocyte
28	273.5	18.3	534	22	AAAB27049	Human amyloid prec
29	273.5	18.3	534	22	AAAB27050	Human amyloid prec
30	273	18.3	340	22	AAU009254	Human B lymphocyte
31	273	18.3	441	22	AAU009055	Human B lymphocyte
32	272.5	18.2	533	22	AAAB93732	Human polypeptide,
33	272.5	18.2	534	22	AAAB88459	Human membrane or
34	271	18.1	387	22	AAAB87415	Human gene 2 encod
35	271	18.1	388	22	AAAB39663	Human polypeptide,
36	271	18.1	1020	22	AAAB39796	Human polypeptide
37	267.5	17.9	244	22	AAU009649	Human B7-H3 polype
38	251	16.8	469	22	AAAB41582	Human polypeptide
39	247	16.5	216	22	AAAB00950	Human B7-H3 polype
40	247	16.5	216	22	AAAB87417	Human gene 2 encod
41	203	13.6	524	19	AAAB64688	Mouse butyrophillin
42	203	13.6	524	20	AAAB78166	Mouse butyrophillin
43	193.5	12.9	524	20	AAAB97815	Guinea pig butyrop
44	185	12.4	329	21	AAV33285	Feline CD86 (B7-2)
45	185	12.4	329	21	AAV33278	Cat CD86 (B7-2) II

ALIGNMENTS

RESULT 1	
AAB08727	
ID	AAB08727 standard; Protein; 288 AA.
XX	
AC	AAB08727;
XX	
DT	02-JAN-2001 (first entry)
XX	
DE	Amino acid sequence of a human B7RP1 polypeptide.
DE	
KW	CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
KW	T-lymphocyte activation; type I transmembrane protein; T cell activation;
KW	T cell proliferation; T-cell mediated disorder.
XX	
OS	Homo sapiens.
XX	
FH	Location/Qualifiers
FT	Peptide
FT	1..16
FT	/note= "signal peptide"
FT	17..288
FT	/note= "mature protein"
FT	259..274
FT	/note= "predicted transmembrane domain"
FT	275..302
FT	/note= "intracellular domain".
XX	
PN	W0200046240-A2.
XX	
PD	10-AUG-2000.
XX	
PE	27-JAN-2000; 2000MO-US01871.
XX	
PR	03-FEB-1999; 99US-0244448.
PR	08-MAR-1999; 99US-0264527.

XX (AMGE-) AMGEN INC.
 PA Yoshinaga SK;
 PI WPI; 2000-543476/49.
 XX N-PSDB; AAA64556.
 DR Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 XX in the treatment, prevention and diagnosis of T cell mediated disorders
 PT
 PS Claim 12; Fig 3A; 174pp; English.
 XX
 PS The present sequence represents a B7RP1 (B7 related protein-1)
 CC polypeptide. The specification also describes a CRP1 (CD28 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX
 SQ Sequence 288 AA;
 Query Match 100.0%; Score 1495; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 6-130;
 Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGSPGLFLFLFSSLRADTQEKVRAMVGSDELSCACPEGSRFDLNDVYVYWTSESK 60
 DB 1 MRGSPGLFLFLFSSLRADTQEKVRAMVGSDELSCACPEGSRFDLNDVYVYWTSESK 60
 QY 61 TVVYTHIPQSSLENDVSRYNRRLMSPAGMLRGDFSLRLEFNTPODEQKFCFLVLSQSL 120
 DB 61 TVVYTHIPQSSLENDVSRYNRRLMSPAGMLRGDFSLRLEFNTPODEQKFCFLVLSQSL 120
 QY 121 GFOEVLSEVTLHVAANFSVPVVSAPHSPODELFTCTSTNGYPRPNVYWIKNIDNSL 180
 DB 121 GFOEVLSEVTLHVAANFSVPVVSAPHSPODELFTCTSTNGYPRPNVYWIKNIDNSL 180
 QY 181 DQALQNDTVFLNMRGLYDVSVLRARTPSVNICCIENVLQONLTVGSQTGNDIGERD 240
 DB 181 DQALQNDTVFLNMRGLYDVSVLRARTPSVNICCIENVLQONLTVGSQTGNDIGERD 240
 QY 241 KITENPVSTGEKNATWSILAVLCLLVVAVAIQWVCRCRCLQHSYAG 288
 DB 241 KITENPVSTGEKNATWSILAVLCLLVVAVAIQWVCRCRCLQHSYAG 288

RESULT 2
 AAB08729
 ID AAB08729 standard; protein; 302 AA.
 XX
 AC AAB08729;
 DT 02-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of a human B7RP1 polypeptide.
 KW CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
 KW T-lymphocyte activation; type I transmembrane protein; T cell activation;
 KW T cell proliferation; T-cell mediated disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT 1..16 Location/Qualifiers
 FT /note= "signal peptide"
 FT Protein 17..302
 FT /note= "polypeptide"
 XX

PN WO200046240-A2.
 XX
 PD 10-AUG-2000.
 XX
 PF 27-JAN-2000; 2000WO-US01871.
 XX
 PR 03-FEB-1999; 99US-0244448.
 PR 08-MAR-1999; 99US-0264527.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Yoshinaga SK;
 XX
 DR WPI; 2000-543476/49.
 DR N-PSDB; AAA64557.
 XX
 PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 PT in the treatment, prevention and diagnosis of T cell mediated disorders
 PS
 PS Claim 12; Fig 12A; 174pp; English.
 XX
 PS The present sequence represents a B7RP1 (B7 related protein-1)
 CC polypeptide. The specification also describes a CRP1 (CD28 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX
 SQ Sequence 302 AA;
 Query Match 100.0%; Score 1495; DB 21; Length 302;
 Best Local Similarity 100.0%; Pred. No. 7e-130;
 Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGSPGLFLFLFSSLRADTQEKVRAMVGSDELSCACPEGSRFDLNDVYVYWTSESK 60
 DB 1 MRGSPGLFLFLFSSLRADTQEKVRAMVGSDELSCACPEGSRFDLNDVYVYWTSESK 60
 QY 61 TVVYTHIPQSSLENDVSRYNRRLMSPAGMLRGDFSLRLEFNTPODEQKFCFLVLSQSL 120
 DB 61 TVVYTHIPQSSLENDVSRYNRRLMSPAGMLRGDFSLRLEFNTPODEQKFCFLVLSQSL 120
 QY 121 GFOEVLSEVTLHVAANFSVPVVSAPHSPODELFTCTSTNGYPRPNVYWIKNIDNSL 180
 DB 121 GFOEVLSEVTLHVAANFSVPVVSAPHSPODELFTCTSTNGYPRPNVYWIKNIDNSL 180
 QY 181 DQALQNDTVFLNMRGLYDVSVLRARTPSVNICCIENVLQONLTVGSQTGNDIGERD 240
 DB 181 DQALQNDTVFLNMRGLYDVSVLRARTPSVNICCIENVLQONLTVGSQTGNDIGERD 240
 QY 241 KITENPVSTGEKNATWSILAVLCLLVVAVAIQWVCRCRCLQHSYAG 288
 DB 241 KITENPVSTGEKNATWSILAVLCLLVVAVAIQWVCRCRCLQHSYAG 288

RESULT 3
 AAG67292
 ID AAG67292 standard; Protein; 302 AA.
 XX
 AC AAG67292;
 DT 13-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of a human hB7-H2 polypeptide.
 KW hB7-H2; T cell stimulator; immunosuppression; cancer; AIDS;
 KW congenital immune deficiency; cellular immune response;
 KW inflammatory condition; autoimmune disease; rheumatoid arthritis;
 KW multiple sclerosis; insulin-dependent diabetes mellitus.

XX Homo sapiens.
OS
XX
XX Key
FH 1..21
FT /note= "signal peptide"
FT 27..135
FT /note= "IgV-like domain"
FT 136..248
FT /note= "IgC-like domain"
FT Domain
PN MO200164704-A1.
PD 07-SEP-2001.
XX
XX 02-MAR-2001; 2001WO-US06769.
XX
XX 02-MAR-2000; 2000US-0186519.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
XX Chen L;
XX
XX MPI: 2001-514837/56.
DR N-PSDB; AAF77869, AAF77870.
XX
XX An isolated DNA encoding a hb7-H2 polypeptide, useful for treating
PT cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis,
PT multiple sclerosis or insulin-dependent diabetes mellitus) -
XX
XX Claim 2; Fig 1A; 50pp; English.
XX
XX The present sequence represents a human polypeptide, designated hb7-H2.
CC The hb7-H2 polypeptide co-stimulates T cells. The hb7-H2 proteins and its
CC variants are generally useful as immune response-stimulating
CC therapeutics. For example, the polypeptides can be used for treatment
CC of disease conditions characterized by immunosuppression, e.g., cancer,
CC AIDS or AIDS-related complex, other virally or environmentally-induced
CC conditions, and certain congenital immune deficiencies. They may also
CC be employed to increase immune function that has been impaired by the
CC use of radiotherapy or immunosuppressive drugs such as certain
CC chemotherapeutic agents, and therefore are particularly useful when
CC given in conjunction with such drugs or radiotherapy. The hb7-H2
CC nucleic acid and polypeptide can be used to treat conditions
CC involving cellular immune responses, e.g., inflammatory conditions
CC (such as, for example, those induced by infectious agents including
CC Mycobacterium tuberculosis or M. leprae), or other pathologic
CC cell-mediated responses such as those involved in autoimmune diseases
CC (e.g. rheumatoid arthritis), multiple sclerosis, or insulin-dependent
CC diabetes mellitus).
XX
XX Sequence 302 AA;
SQ
Query Match 100.0%; Score 1495; DB 22; Length 302;
Best Local Similarity 100.0%; Pred. No. 7e-130;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGSPGLFLFLFSSLRADTOEKEVRAMVGSDELSCACPEGSREFDLNDVYVYQTSSEK 60
DB 1 MRGSPGLFLFLFSSLRADTOEKEVRAMVGSDELSCACPEGSREFDLNDVYVYQTSSEK 60
QY 61 TVVYTHIPONSSLENDVSRNRALMSPAGMLRGDFSLRLFNVTPODEQKPHCLVLSQSL 120
DB 61 TVVYTHIPONSSLENDVSRNRALMSPAGMLRGDFSLRLFNVTPODEQKPHCLVLSQSL 120
QY 121 GROEVLSEVETLHVAAANFSVPVVSAPHSPQDELFTCTSIINGYPRPNVYWKNTDMSL 180
DB 121 GROEVLSEVETLHVAAANFSVPVVSAPHSPQDELFTCTSIINGYPRPNVYWKNTDMSL 180
QY 181 DQALQNDTVFLNMRGLYDVSVLRIARTPSVNICCIENVLQOQLTVGSOTGNDIGERD 240
DB 181 DQALQNDTVFLNMRGLYDVSVLRIARTPSVNICCIENVLQOQLTVGSOTGNDIGERD 240

QY 241 KITEPNVSTGEKNATWSIIAIVLCILVYVAVAIGWCRDRCLQHSYAG 288
DB 241 KITEPNVSTGEKNATWSIIAIVLCILVYVAVAIGWCRDRCLQHSYAG 288
RESULT 4
AAB67713
ID AAB67713 standard; Protein; 309 AA.
AC AAB67713;
XX
XX 11-JUN-2001 (first entry)
DE
XX Amino acid sequence of a human GL50 polypeptide.
DE
XX GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
KW acquired immune deficiency syndrome; AIDS; vaccine.
XX
XX Homo sapiens.
XX
XX MO200121796-A2.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-US25892.
XX
XX 21-SEP-1999; 99US-0155043.
XX
XX (GEMX) GENETICS INST INC.
XX
XX Ling V, Dunussi-Joannopoulos K;
XX
XX MPI: 2001-244938/25.
DR N-PSDB; AAF79921.
XX
XX New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT immune response and reducing the proliferation of a tumour cell -
XX
XX Claim 13; Fig 8; 195pp; English.
XX
XX The present sequence represents a human GL50 polypeptides. GL50
CC molecules are antigens on the surface of antigen presenting cells,
CC which costimulate T cell proliferation and bind to costimulatory
CC receptor ligands on T cells. GL50 modulating agents are used to
CC modulate an immune response in a subject. GL50 polypeptides are used
CC to modulate T cell costimulation, and to reduce the proliferation of
CC a tumour cell. Diseases that can be treated using GL50 molecules are
CC graft-versus-host disease, autoimmune disease, allergies, acquired
CC immune deficiency syndrome (AIDS), and viral infections. The GL50
CC molecules can be used in vaccines. GL50 polynucleotides can be used
CC to locate gene regions associated with genetic disease, in tissue
CC typing, and in forensic identification of a biological sample.
XX
XX Sequence 309 AA;
SQ
Query Match 100.0%; Score 1495; DB 22; Length 309;
Best Local Similarity 100.0%; Pred. No. 7.2e-130;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGSPGLFLFLFSSLRADTOEKEVRAMVGSDELSCACPEGSREFDLNDVYVYQTSSEK 60
DB 1 MRGSPGLFLFLFSSLRADTOEKEVRAMVGSDELSCACPEGSREFDLNDVYVYQTSSEK 60
QY 61 TVVYTHIPONSSLENDVSRNRALMSPAGMLRGDFSLRLFNVTPODEQKPHCLVLSQSL 120
DB 61 TVVYTHIPONSSLENDVSRNRALMSPAGMLRGDFSLRLFNVTPODEQKPHCLVLSQSL 120
QY 121 GROEVLSEVETLHVAAANFSVPVVSAPHSPQDELFTCTSIINGYPRPNVYWKNTDMSL 180
DB 121 GROEVLSEVETLHVAAANFSVPVVSAPHSPQDELFTCTSIINGYPRPNVYWKNTDMSL 180
QY 181 DQALQNDTVFLNMRGLYDVSVLRIARTPSVNICCIENVLQOQLTVGSOTGNDIGERD 240
DB 181 DQALQNDTVFLNMRGLYDVSVLRIARTPSVNICCIENVLQOQLTVGSOTGNDIGERD 240

```

Db 181 DOALQNDTVFLNMRGLDYVSVLRIRTPSVNIGCCIEENVLLQONLTVGSQTGNDIGERD 240
QY 241 KITEPNVSTGEKNAAWTSLIAVLCLLVYVAIVAIGWCRDRCLQHSYAG 288
Db 241 KITEPNVSTGEKNAAWTSLIAVLCLLVYVAIVAIGWCRDRCLQHSYAG 288

RESULT 5
AAU00422
ID AAU00422 standard; Protein; 516 AA.
XX
XX AAU00422;
XX
XX 11-MAY-2001 (first entry)
XX
XX Human B7-3 protein.
XX
XX Human; B7-3; Inducible co-stimulator; ICOS; TU-D; KIAA0653; CD28;
XX T-cell; ICOS-mediated activity; IL-10 production; TH2 activity;
XX Helicobacter pylori induced peptic ulcer; Crohn's disease;
XX Multiple sclerosis; type I diabetes mellitus; graft rejection;
XX helminth infection; allergic disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH Binding-site 49..56
XX FT /note= "Beta-strand C sequence useful in the design of
XX FT inhibitors of the interaction of B7-3 with ICOS"
XX FT Binding-site 60..67
XX FT /note= "Beta-strand C' sequence useful in the design of
XX FT inhibitors of the interaction of B7-3 with ICOS"
XX FT Binding-site 73..77
XX FT /note= "Beta-strand C" sequence useful in the design of
XX FT inhibitors of the interaction of B7-3 with ICOS"
XX FT Binding-site 109..118
XX FT /note= "Beta-strand F sequence useful in the design of
XX FT inhibitors of the interaction of B7-3 with ICOS"
XX FT Binding-site 121..134
XX FT /note= "Beta-strand G sequence useful in the design of
XX FT inhibitors of the interaction of B7-3 with ICOS"
XX
XX WO200112658-A2.
XX
XX 22-FEB-2001.
XX
XX 10-AUG-2000; 2000WO-GB03079.
XX
XX 11-AUG-1999; 99US-0148402.
XX
XX (ISIS-) ISIS INNOVATIONS LTD.
XX
XX PA
XX PI Davis S;
XX DR WPI; 2001-226547/23.
XX DR N-PSDB; AAS00423.
XX
XX New B7-3 polypeptides useful for modulating inducible co-stimulator
XX protein and for treating ulcers, Crohn's disease, multiple sclerosis,
XX diabetes mellitus, infections and allergic diseases
XX
XX Claim 1; Page 68; 77pp; English.
XX
XX The present sequence represents a novel human B7-3 protein which acts
XX as a ligand for inducible co-stimulator (ICOS) protein. The B7-3 protein
XX previously referred to as TU-D or KIAA0653 was considered by the 2
XX groups as being incomplete. The present inventor has determined the
XX sequence to be complete and renamed the sequence as B7-3. Also described
XX is a soluble form of B7-3 (AAU00423) which comprises the B7-3 signal to
XX sequence and extracellular domain. The extracellular domain is shown to
XX bind ICOS which is related to CD28 and expressed on T-cells. B7-3
XX polypeptides or its fragments are useful for identifying a substance

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CC which interacts with the polypeptide or its fragment. B7-3 polypeptides,
CC fragments, tetramer, an agent with an ability to affect B7-3 activity or
CC a specific binding member are useful for modulating an ICOS-mediated
CC activity of T-cells by modulating IL-10 production and TH2 activity, and
CC for manufacturing a medicament for modulating an ICOS-mediated activity
CC of T-cells. B7-3 polypeptides are useful for development of diagnostic,
CC prophylactic and therapeutic agents for diseases such as Helicobacter
CC pylori induced peptic ulcers, Crohn's disease, multiple sclerosis, type
CC I diabetes mellitus, graft rejection, helminth infections, and allergic
CC diseases.
XX
XX Sequence 516 AA;
XX
XX Query Match 100.0%; Score 1495; DB 22; Length 516;
XX Best Local Similarity 100.0%; Pred. No. 1.5e-129;
XX Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLGSPGILLFLFFSLRADTQKEVRAVNGSDVELSCACPEGSFEDINDVYVWQTSSEK 60
Db 1 MRLGSPGILLFLFFSLRADTQKEVRAVNGSDVELSCACPEGSFEDINDVYVWQTSSEK 60
QY 61 TVVYTHIPQNSLSENVDSRYRNRRLMSPAGLRDFTSLRFNVPDQEFHCLVLSQSL 120
Db 61 TVVYTHIPQNSLSENVDSRYRNRRLMSPAGLRDFTSLRFNVPDQEFHCLVLSQSL 120
QY 121 GFOEVLSEVTLHVAANFSPVVSAPHSQSDELFTCTTSINGYPRPNVWINKTNSLL 180
Db 121 GFOEVLSEVTLHVAANFSPVVSAPHSQSDELFTCTTSINGYPRPNVWINKTNSLL 180
QY 181 DOALQNDTVFLNMRGLDYVSVLRIRTPSVNIGCCIEENVLLQONLTVGSQTGNDIGERD 240
Db 181 DOALQNDTVFLNMRGLDYVSVLRIRTPSVNIGCCIEENVLLQONLTVGSQTGNDIGERD 240
QY 241 KITEPNVSTGEKNAAWTSLIAVLCLLVYVAIVAIGWCRDRCLQHSYAG 288
Db 241 KITEPNVSTGEKNAAWTSLIAVLCLLVYVAIVAIGWCRDRCLQHSYAG 288

RESULT 6
ABBI0322
ID ABBI0322 standard; Protein; 343 AA.
XX
XX AC ABBI0322;
XX
XX 10-JAN-2002 (first entry)
XX
XX Human cDNA SEQ ID NO: 630.
XX
XX Human; gene therapy; neural disorder; immune system disorder;
XX muscular disorder; reproductive disorder; gastrointestinal disorder;
XX pulmonary disorder; cardiovascular disorder; renal disorder;
XX proliferative disorder; inflammation.
XX
XX Homo sapiens.
XX
XX WO200154474-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01349.
XX
XX 31-JAN-2000; 2000US-179065P.
XX 04-FEB-2000; 2000US-180628P.
XX 24-FEB-2000; 2000US-184664P.
XX 02-MAR-2000; 2000US-186350P.
XX 16-MAR-2000; 2000US-189874P.
XX 17-MAR-2000; 2000US-190076P.
XX 18-APR-2000; 2000US-198123P.
XX 19-MAY-2000; 2000US-205515P.
XX 07-JUN-2000; 2000US-209467P.
XX 28-JUN-2000; 2000US-214886P.
XX 30-JUN-2000; 2000US-215135P.
XX 07-JUL-2000; 2000US-216647P.

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PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225213P.
PR 14-AUG-2000; 2000US-225214P.
PR 14-AUG-2000; 2000US-225266P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 14-AUG-2000; 2000US-225759P.
PR 18-AUG-2000; 2000US-226279P.
PR 22-AUG-2000; 2000US-226681P.
PR 22-AUG-2000; 2000US-226688P.
PR 22-AUG-2000; 2000US-227182P.
PR 23-AUG-2000; 2000US-227009P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
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(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476161/51.
DX N-PSDB; ABA06544.
DR
XX
XX Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition -
PT
XX
XX
XX Claim 11; SEQ ID NO: 630; 859pp + Sequence Listing; English.
XX
XX
XX The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention.
XX
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PA	(HUMA-)	HUMAN GENOME SCI INC.	PA	(HUMA-)	HUMAN GENOME SCI INC.
PI	Rosen CA,	Barash SC, Ruben SK;	PI	Rosen CA,	Barash SC, Ruben SK;
XX			XX		
DR	WPI: 2001-476161/51.		DR	WPI: 2001-476161/51.	
DR	N-PSDB: ABA06724.		DR	N-PSDB: ABA06724.	
XX			XX		
PT	Isolated nucleic acid molecule encoding an inflammation-associated		PT	Isolated nucleic acid molecule encoding an inflammation-associated	
PT	polypeptide is used in preventing, treating or ameliorating a medical		PT	polypeptide is used in preventing, treating or ameliorating a medical	
PT	condition -		PT	condition -	
XX			XX		
PS	Claim 11; SEQ ID NO: 810; 859pp + Sequence Listing; English.		PS	Claim 11; SEQ ID NO: 810; 859pp + Sequence Listing; English.	
XX			XX		
CC	The present invention provides human cDNAs, proteins and related genomic		CC	The present invention provides human cDNAs, proteins and related genomic	
CC	DNAs. These can be used in the treatment of neural, immune system,		CC	DNAs. These	

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Kw	antileusar therapy; gene therapy; neurological disorder; renal disorder		
Kw	cardiovascular disorder; gastrointestinal disorder; pulmonary disorder		
Kw	reproductive disorder; immune system disorder; proliferative disorder;		
XX	muscular disorder.		
XX	Homo sapiens.		
XX	WO200155315-A2.		
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XX
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XX
DT 07-NOV-2001 (first entry)
XX
DP Human immunoglobulin polypeptide SEQ ID No 150.
XX
KW Immunoglobulin; signal transduction pathway protein; cancer;
KW antileukemia therapy; gene therapy; neurological disorder; renal disorder;
KW cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;
KW reproductive disorder; immune system disorder; proliferative disorder;
KW muscular disorder.
XX
OS Homo sapiens.
XX
PN WO200155315-A2.
XX
PD 02-AUG-2001.
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 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-457725/49.
 DR N-PSDB; AAS28793.
 XX
 PT Isolated novel immunoglobulin polypeptide for monitoring the presence
 PT and progression of diseases and for diagnosis -
 XX
 PS Claim 11: SEQ ID No 150; 551bp; English.
 XX
 XX Sequences AAU17977-AAU18087 represent immunoglobulin polypeptides of the
 CC invention. The polypeptides and their associated polynucleotides can be
 CC used to diagnose a pathological condition or a susceptibility to a
 CC pathological condition in a subject by determining the presence or
 CC absence of a mutation in a DNA sequence or determining the presence or
 CC amount of expression of the protein. Alternatively the identification of
 CC a binding partner to a sequence allows determination of changes in
 CC protein activity. The sequences can be used as research tools for
 CC receptors or other signal transduction pathway proteins that interact
 CC with the polypeptides of the invention and can be used to treat, prevent
 CC or diagnose various types of disorders such as neurological disorders,
 CC cardiovascular disorders, gastrointestinal disorders, reproductive
 CC disorders, immune system disorders, renal disorders, muscular disorders,
 CC pulmonary disorders, proliferative disorders and cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
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 SO Sequence 370 AA:
 Query Match 99.9%; Score 1494; DB 22; Length 370;
 Best Local Similarity 99.7%; Pred. No. 1,le-129;
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 QY 241 KITENPVSTGEKNAATWSILAVLCILVYVAVAIGWVCHDRCLQHSYAG 288
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 DB 309 KITENPVSTGEKNAATWSILAVLCILVYVAVAIGWVCHDRCLQHSYAG 356
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 ID AAB87395 standard; Protein; 302 AA.
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 AC AAB87395;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Human gene 2 encoded secreted protein HMWDB84, SEQ ID NO:136.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiotensin disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulnerability;
 KW cell culture; chemotaxis; food additive;
 KW binding partner identification.
 KW
 OS Homo sapiens.
 XX
 PN WO200118022-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US24008.
 XX
 PR 03-SEP-1999; 99US-0152315.
 PR 03-SEP-1999; 99US-0152317.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ni J, Baker KP, Birse CE, Fiscella M, Komatsu GA, Rosen CA;
 PI Soppet DR, Young PE, Ehner R, Duan DR, Olsen HS, Lafleur DW;
 PI Moore PA, Shi Y, Wei Y, Florence KA;
 XX
 DR WPI: 2001-203081/20.
 DR N-PSDB; AAF91911.
 XX
 PT Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers -
 XX
 PS Claim 11: Page 564-565; 607bp; English.
 XX
 XX AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted
 CC protein genes, and AAB87342-AAB87413 represent the proteins they encode.
 CC AAB87414-AAB87454 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 52 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,

PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225477.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.

PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250161.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPT, 2001-457725/49.
N-PSDB; AAS28855.

Isolated novel immunoglobulin polypeptide for monitoring the presence
and progression of diseases and for diagnosis -

Claim 11; SEQ ID No 212; 551pp; English.

Sequences AAU17977-AAU18087 represent immunoglobulin polypeptides of the
invention. The polypeptides and their associated polynucleotides can be
used to diagnose a pathological condition or a susceptibility to a
pathological condition in a subject by determining the presence or
absence of a mutation in a DNA sequence or determining the presence or
amount of expression of the protein. Alternatively the identification of
a binding partner to a sequence allows determination of changes in
protein activity. The sequences can be used as research tools for
receptors or other signal transduction pathway proteins that interact
with the polypeptides of the invention and can be used to treat, prevent
or diagnose various types of disorders such as neurological disorders,
cardiovascular disorders, gastrointestinal disorders, reproductive
disorders, immune system disorders, renal disorders, muscular disorders,
CC pulmonary disorders, proliferative disorders and cancer.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.


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XX  MO200121796-A2.
PN
XX
XX  29-MAR-2001.
PD
XX
XX  21-SEP-2000; 2000WO-US25892.
PF
XX  21-SEP-1999; 99US-0155043.
PR
XX  (GEMV ) GENETICS INST INC.
PA
XX  Ling V, Dunuss-Ioannopolulos K;
PI
XX  WPI; 2001-244938/25.
DR  N-PSDB; AAF79941.
XX
XX  New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT  immune response and reducing the proliferation of a tumour cell -
XX
XX  Disclosure; Fig 28B; 195pp; English.
PS
XX  The present sequence represents a fusion protein, comprising human GL50
CC  (hGL50) and murine IgG2a (mig2a). The fusion protein is used in the
CC  course of the invention. The specification describes GL50 polypeptides.
CC  GL50 molecules are antigens on the surface of antigen presenting cells,
CC  which costimulate T cell proliferation and bind to costimulatory receptor
CC  ligands on T cells. GL50 modulating agents are used to modulate T cell
CC  response in a subject. GL50 polypeptides are used to modulate T cell
CC  costimulation, and to reduce the proliferation of a tumour cell. Diseases
CC  that can be treated using GL50 molecules are graft-versus-host disease,
CC  autoimmune disease, allergies, acquired immune deficiency syndrome
CC  (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
CC  GL50 polynucleotides can be used to locate gene regions associated with
CC  genetic disease, in tissue typing, and in forensic identification of a
XX  biological sample.
XX
XX  Sequence 490 AA;
SQ
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XX  Query Match 81.5%; Score 1218; DB 22; Length 490;
XX  Best local Similarity 96.3%; Pred. No. 5.4e-104;
XX  Matches 237; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
QY  8 LLEFLFSLRADDOKEKVRAMVSGDVELSCACPEGSFEDLNDVYVYQTSSEKTVYTH 67
DB  14 VLALFPSMA--SMEKVRAMVSGDVELSCACPEGSFEDLNDVYVYQTSSEKTVYTH 71
QY  68 PONSLENVDSRYNRRLAMSPAGMLRGDFSLRLFNVPPOEOKFHCVLVSQSIGFQEVLS 127
DB  72 PONSLENVDSRYNRRLAMSPAGMLRGDFSLRLFNVPPOEOKFHCVLVSQSIGFQEVLS 131
QY  128 VEVTLHVAANFSVPVSAHPSPODELFTCTSTINGYPRPNVYWIKNKDNSLLDQALOND 187
DB  132 VEVTLHVAANFSVPVSAHPSPODELFTCTSTINGYPRPNVYWIKNKDNSLLDQALOND 191
QY  188 TVEFLNMGIDVYVSLRLARTPSVNICCTENVLQONLTVSGTGDIERKRTENPV 247
DB  192 TVEFLNMGIDVYVSLRLARTPSVNICCTENVLQONLTVSGTGDIERKRTENPV 251
QY  248 STGEKN 253
DB  252 STGEKN 257
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XX  RESULT 15
XX  AAB08725
ID  AAB08725 standard; Protein; 322 AA.
XX
XX  AAB08725;
AC
XX  02-JAN-2001 (first entry)
DT
XX  Amino acid sequence of a murine B7Rp1 polypeptide.
DE
XX

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KM  CRP1; CD28 related protein-1; B7Rp1; B7 related protein-1;
KM  T-lymphocyte activation; type I transmembrane protein; T cell activation;
KM  T cell proliferation; T-cell mediated disorder.
XX
XX  Mus sp.
OS
XX
XX  Key
FH  Peptide
FT  1..46
FT  /note= "signal peptide"
FT  47..322
FT  Protein
FT  /note= "mature protein"
FT  47..279
FT  Domain
FT  /note= "extracellular domain"
FT  280..298
FT  /note= "predicted transmembrane domain"
FT  299..322
FT  Domain
FT  /note= "intracellular domain"
XX
XX  WO20046240-A2.
PN
XX
XX  10-AUG-2000.
PD
XX
XX  27-JAN-2000; 2000WO-US01871.
XX
XX  03-FEB-1999; 99US-0244448.
XX  08-MAR-1999; 99US-0264527.
XX
XX  (AMGE-) AMGEN INC.
PA
XX
XX  Yoshinaga SK;
PI
XX
XX  WPI; 2000-543476/49.
DR
XX  N-PSDB; AAA64555.
XX
XX  Novel nucleic acids encoding the proteins CRP-1 and B7Rp1 are useful
PT  in the treatment, prevention and diagnosis of T cell mediated disorders
PT
XX
XX  Claim 12; Fig 2a; 174pp; English.
PS
XX
XX  The present sequence represents a B7Rp1 (B7 related protein-1)
CC  polypeptide. The specification also describes a CRP1 (CD28 related
CC  protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
CC  activation, and represent a receptor-ligand pair. CRP1 and B7Rp1 are
CC  predicted to be a type I transmembrane protein. The nucleic acids are
CC  useful for regulating T cell activation or proliferation in an animal.
CC  The polypeptides are useful for treating, preventing ameliorating or
CC  diagnosing a T-cell mediated disorder in an animal. They can also be
XX  used to identify test molecules that bind to the polypeptides.
XX
XX  Sequence 322 AA;
SQ
XX
XX  Query Match 39.4%; Score 588.5; DB 21; Length 322;
XX  Best local Similarity 46.6%; Pred. No. 4.6e-46;
XX  Matches 135; Conservative 39; Mismatches 97; Indels 19; Gaps 7;
QY  7 GLLEFLFSLRADDOKEKVRAMVSGDVELSCACPEGSFEDLNDVYVYQTSSEKTVYTH 66
DB  32 GLLEFLFSLRADDOKEKVRAMVSGDVELSCACPEGSFEDLNDVYVYQTSSEKTVYTH 91
QY  67 IPONSLENVDSRYNRRLAMSPAGMLRGDFSLRLFNVPPOEOKFHCVLVSQSIGFQEV 125
DB  92 LPKSPGIVNDSSYKRNKRLHSLDSMKQGFSLYLNVPPOEOKFHCVLVSQSIGFQEV 151
QY  126 LSEVETLHVAANFSVPVSAHPSPODELFTCTSTINGYPRPNVYWIKNKDNSLLDQAL 183
DB  152 LSEVETLHVAANFSVPVSAHPSPODELFTCTSTINGYPRPNVYWIKNKDNSLLDQAL 210
QY  184 LONDVFLNMGIDVYVSLRLARTPSVNICCTENVLQONLTVSGTGDIERKRTENPV 239
DB  211 LONDVFLNMGIDVYVSLRLARTPSVNICCTENVLQONLTVSGTGDIERKRTENPV 266
QY  240 DKITENPVSTGEKNATWLSILAVLCILVYVAVALGWCRDRCLQH-STAG 288

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Wed Oct 23 13:57:48 2002

us-09-728-420c-12.rag

Page 16

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GenCore version 5.1.3
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OM protein - protein search, using sw model

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Title: US-09-728-420c-12

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	12.2	309	2 US-08-456-104-4	Sequence 4, Appl
2	182	12.2	309	4 US-08-479-744A-23	Sequence 23, Appl
3	182	12.2	309	4 US-08-280-757B-23	Sequence 23, Appl
4	182	12.2	309	4 US-08-205-697A-21	Sequence 21, Appl
5	182	12.2	309	4 US-08-702-525-21	Sequence 21, Appl
6	182	12.2	309	5 PCT-US95-02576-21	Sequence 13, Appl
7	182	12.2	314	4 US-08-205-697A-13	Sequence 13, Appl
8	182	12.2	314	4 US-08-702-525-13	Sequence 13, Appl
9	182	12.2	314	5 PCT-US95-02576-13	Sequence 13, Appl
10	173	11.6	589	2 US-08-724-394A-1	Sequence 13, Appl
11	165.5	11.1	323	5 PCT-US94-09642-2	Sequence 2, Appl
12	165.5	11.1	329	2 US-08-456-104-2	Sequence 2, Appl
13	165.5	11.1	329	2 US-08-101-624-2	Sequence 2, Appl
14	165.5	11.1	329	3 US-08-479-744A-2	Sequence 2, Appl
15	165.5	11.1	329	4 US-08-280-757B-2	Sequence 2, Appl
16	165.5	11.1	329	4 US-08-205-697A-23	Sequence 23, Appl
17	165.5	11.1	329	4 US-08-702-525-23	Sequence 23, Appl
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20	164.5	11.0	288	2 US-08-147-772-2	Sequence 2, Appl
21	164.5	11.0	288	2 US-08-456-104-6	Sequence 6, Appl
22	164.5	11.0	288	2 US-08-101-624-23	Sequence 23, Appl
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25	164.5	11.0	288	3 US-08-479-744A-29	Sequence 29, Appl
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27	164.5	11.0	288	4 US-09-159-135-2	Sequence 2, Appl

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33	161	10.8	208	4 US-09-460-384-36	Sequence 36, Appl
34	161	10.8	473	4 US-09-171-945-131	Sequence 131, Appl
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36	158	10.6	208	4 US-09-375-419-15	Sequence 15, Appl
37	152	10.2	320	4 US-08-205-697A-2	Sequence 2, Appl
38	152	10.2	320	4 US-08-702-525-2	Sequence 2, Appl
39	152	10.2	320	5 PCT-US95-02576-2	Sequence 2, Appl
40	151.5	10.1	306	4 US-08-205-697A-17	Sequence 17, Appl
41	151.5	10.1	306	4 US-08-702-525-17	Sequence 17, Appl
42	151.5	10.1	306	5 PCT-US95-02576-17	Sequence 17, Appl
43	147	9.8	342	2 US-08-724-394A-6	Sequence 6, Appl
44	144.5	9.7	306	2 US-08-147-772-4	Sequence 4, Appl
45	144.5	9.7	306	2 US-08-456-104-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-456-104-4
; Sequence 4, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandagouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-104-4
Query Match 12.2%, Score 182; DB 2; Length 309;
Best Local Similarity 23.6%, Pred. No. 3e-10;
Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14;

US-08-479-744A-23
Sequence 23, Application US/08479744A

12.28; Score 182; DB 3; Length 309;

RESULT 3
US-08-280-757B-23
; Sequence 23, Application US/08280757B

US-08-280-757B-23

[illegible]

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RESULT 4
US-08-205-697A-21
; Sequence 21, Application US/08205697A
; Patent No. 6218510
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/205.697A
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-205-697A-21
;
Query Match 12.2%; Score 182; DB 4; Length 309;
Best Local Similarity 23.6%; Pred. No. 3e-10;
Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14;

```

Db	8	GLAILFVYLLISDAVSERQAFNGTAYLPCEPFRKAQISLSSELVEMQ--DQKILY	66
Qy	65	YHPQNSLENDSCRIRRMALMSPAGMRGDFSLRLEFNVPDEOKFHLVLSQ----	SL 120
Db	67	EHVLGTERKLDVNAKLGTSFD-----RNNWTLRLHNVAQIKMGSYDCEIQKRPPTGI	122
Qy	121	GFOEVLSEVEVTHLVANESVPAVS-APHSPODELITCTISINGYRP--NYWI--NKT-	175
Db	122	ILQOITL---ELSVIANESEPIKLAQVNTGNSINLTCTSKGHPKPKMYFLITNSTN	176
Qy	176	---DNSLIDQALQNDVFLNMKGVLADVSVYLRARPSY---NGGICENVLQOONLVG	222
Db	179	EYGDNQIISD-----NVELFISINSLISLSPGCVGHMRYVVELT-----ESMKS	222
Qy	230	SQGNIDIGERDKITENPVSTGEKNNAWISLAVLCILLVVAVALGAVWCRCLOQS	285
Db	227	SKPLNFTQE---FSPQYVMEIRIASVYVALVLLMLIT-----VCHRRKNQDS	272

```

US-08-702-525-21
; Sequence 21, Application US/08702525
; Patent No. 629460
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon
; APPLICANT: Nadler, Lee
; TITLE OF INVENTION: No. 629460el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,525
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E,
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWT-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-525-21

Query Match 12.2%; Score 182; DB 4; Length 309;
Best Local Similarity 23.6%; Pred. No. 3e-10;
Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14,

```

```

OY      65 YH1PQNSLELVNDSRYRRALAMPAGMLRGDFSLRLNNVPRDQGRKHCXVLQO---SL 120
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      67 EHY1LCTEKLDVSNAKYLGRTSEF-----RNWWT1RLNNVQIKDNGSDYCTIQKKPPGTST 121
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY      121 GFQEVLYSVETVTLHVAANESVYVS-AEHSPSQDELFTCTSI NGYPRP-NVYWI--NKT- 175
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      122 ILQOQLT---ELSVIANSESEPEIKLAONVNGSINGINTCTSKQCHPRKMYFL1NSTN 178
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY      176 ---DNSLIDQALQNDYFLNRRGLXDVVSYLRARTSY---NIGCCIEVLLQONITVG 229
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      179 EYGDNMQISQD-----NNTLEFSTISNLSISLFEPGVNHWMTVVCLEL---ESMKIS 226
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY      230 SQTGNDIGDERDKITENPVSSTGEKNAATWSILAVLCLELVVAVA1GWVCBDRCLQHS 285
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      227 SKPLNFTQO-----PPSPQTWYMKETTSATVAVALLVMLLI-----VCHKKRPQPS 272
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 6
 PCT-US95-02576-21
 Sequence 21, Application PC/TUS9502576
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
 TITLE OF INVENTION: and Uses Therefor
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/02576
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/205,697
 FILING DATE: 02-Mar-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragouras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: BMT-120CPPC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)227-5941
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 309 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-02576-21

Query Match	12.2%	Score 182:	DB 5:	Length 309:
Best Local Similarity	23.6%:	Pred. No. 3e-10:		
Matches	70:	Conservative	61:	Mismatches 117: Indels 48: Gaps 14:
QY	7	GLLFLFSS--LRADQKEKVRAMGSDVELESCACPEGRSFDLNDVYVYQTSKSTVYV	64	
DB	8	GLALILFVYLLISDASVETQATFNCGATYLPCEPFTKAQNTSLSELVEFWQ--DQAKLVLY	66	
QY	65	YHPIQNSLENDSDRYRNRLALMSGMLRGDFSLRLFNVTYPDQEKHCLVLSQ----	SL 120	
DB	67	EHLTGTEKEDSVNAKYLGRTSFD-----RNMTWTRLRHNVLKIDMGSDYDCEIQKKPPTGSI	121	
QY	121	GPKEVLSVEVTLHVANAFSVPVYS--AHSPSQDELITCTGSIINGYPRP--NVIYI--NKT--	175	
DB	122	ILIQQTTL---ELSVIANSEPEIKIAQVNTGNSGINTLCTSKQGHPRPKMYKVLFLNNSIN	178	

```

QY 176 --DNLSILDLQNLQNTFVLLNRRGLDYVYLRIRRTSY-- --NGCCIEANVLQQLNTFG 229
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 179 EYGDMMQISQD-----NTLFLFSINLSLSLSEFPDGMHMYVYCLT-----ESKIS 226
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 230 SQTGNDIERDKITENPYSTGEKNAATWSILAVICLLVVAVALGWGRDRCIQHS 285
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 227 SKPLNFTQE---PSPQTYMKETASTAVALLVLMILLI-----VCHKRPQPS 272
      | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

      1  RESULT 7
      2  US-08-205-697A-13
      3  ; Sequence 13, Application US/08205697A
      4  ; Patent No. 6218510
      5  ; GENERAL INFORMATION:
      6  ; APPLICANT: Sharpe, Arlene H.
      7  ; APPLICANT: Borriello, Francescopaolo
      8  ; APPLICANT: Freeman, Gordon J.
      9  ; APPLICANT: Nadler, Lee M.
     10  ; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
     11  ; TITLE OF INVENTION: and uses therefor
     12  ; NUMBER OF SEQUENCES: 61
     13  ; CORRESPONDENCE ADDRESSES:
     14  ; ADDRESSEE: LAHIVE & COCKFIELD
     15  ; STREET: 60 State Street, suite 510
     16  ; CITY: Boston
     17  ; STATE: Massachusetts
     18  ; COUNTRY: USA
     19  ; ZIP: 02109-1875
     20  ; COMPUTER READABLE FORM:
     21  ; MEDIUM TYPE: Floppy disk
     22  ; COMPUTER: IBM PC compatible
     23  ; OPERATING SYSTEM: PC-DOS/MS-DOS
     24  ; SOFTWARE: ASCII Text
     25  ; CURRENT APPLICATION DATA:
     26  ; APPLICATION NUMBER: US/08/205,697A
     27  ; FILING DATE: 02-Mar-1994
     28  ; ATTORNEY/AGENT INFORMATION:
     29  ; NAME: Mandragouras, Amy E.
     30  ; REGISTRATION NUMBER: 36,207
     31  ; REFERENCE/DOCKET NUMBER: BWT-120
     32  ; TELECOMMUNICATION INFORMATION:
     33  ; TELEPHONE: (617)227-7400
     34  ; TELEFAX: (617)227-5941
     35  ; INFORMATION FOR SEQ. ID NO: 13:
     36  ; SEQUENCE CHARACTERISTICS:
     37  ; LENGTH: 314 amino acids
     38  ; TYPE: amino acid
     39  ; TOPOLOGY: linear
     40  ; MOLECULE TYPE: protein
     41  ;
     42  ; US-08-205-697A-13

```

[illegible]


```

? APPLICANT: Kronmal, Gregory S.
? APPLICANT: Lauer, Peter M.
? APPLICANT: Ruddy, David A.
? APPLICANT: Thomas, Winston
? APPLICANT: Tsuchihashi, Zenta
? APPLICANT: Wolff, Roger K.
? TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
? TITLE OF INVENTION: Sequences and Antibodies Thereo
? NUMBER OF SEQUENCES: 31
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: TOWNSEND and CREW LLP
? STREET: Two Embarcadero Center, 8th Floor
? CITY: San Francisco
? STATE: CA
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/724,394A
? FILING DATE: 01-OCT-1996
? CLASSIFICATION: 536
? ATTORNEY/AGENT INFORMATION:
? NAME: Filts, Renee A.
? REGISTRATION NUMBER: 35,136
? REFERENCE/DOCKET NUMBER: 01957-000100
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-576-0200
? TELEFAX: 415-576-0300
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 589 amino acids
? TYPE: amino acid
? STRANDEDNESS: not relevant
? TOPOLOGY: not relevant
? MOLECULE TYPE: peptide
? FEATURE:
? NAME/KEY: Region
? LOCATION: 1..589
? OTHER INFORMATION: /note="BT"
? US-08-724-394A-1

Query Match 11.6%; Score 173; DB 2; Length 589;
Best Local Similarity 23.7%; Pred. No. 6.2e-09;
Matches 64; Conservative 36; Mismatches 126; Indels 44; Gaps 8;

25 VRAMGSDVELSC-ACPEGRDPLNDVYVYMQTSEKTYVTHIFQNSSLENDVSRYYR 83
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 41 ILAVVEDELPCRLSPNASHLE--LRWFRKKVSPAVLVHRDGRDEAEQMPERYGR 97
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 84 ALMSPGMLRGDFSLRLFVNTPODEQKFLVLQSLSGFQEVLSVEVTLHVANFSPVY 143
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 98 ATLVDGIAKGRVALRIRREVRSDOGEYCF-FREDSYTEAL--VHLKVAALGSDPHI 153
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 144 SAPHSSQDELFTFTCTSINGYPRPNVYVWINKTDSLLDQALONDVFLNMRGLYDVSVL 203
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 154 SM-QVOEENGEICLECTSVMPPEQVOWRTSGKEKFPSTESRNP--DEECLFVAASV 209
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 204 RIARFSPVNICCIENVLLQONLVGSSQGNIGERDKITENPVSTGKNAATW----- 257
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 210 IIRDTSTKAVSCYIOWLL-----GQEKVEISIPASSLPRLTPWIVAVAV 255
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 258 -----SILAVLCILVVAVAIQW 275
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 256 XXXXXXXXXXILMVLGILITGSIFFTW 285
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 11
PCT-US94-09642-2
; Sequence 2, Application PC/TUS9409642
```

```

? GENERAL INFORMATION:
? APPLICANT:
? TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
? TITLE OF INVENTION: Protein and Related Reagents
? NUMBER OF SEQUENCES: 2
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Schering-Plough Corporation, M-3-W
? STREET: One Giralda Farms
? CITY: Madison
? STATE: New Jersey
? COUNTRY: USA
? ZIP: 07940-1000
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: Apple Macintosh IIcx
? OPERATING SYSTEM: System Software 7.1
? SOFTWARE: Microsoft Word 5.1a
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US94/09642
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/120,606
? FILING DATE: 13-SEP-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/116,882
? FILING DATE: 03-SEP-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Blasdale, John H. C.
? REGISTRATION NUMBER: 31,895
? REFERENCE/DOCKET NUMBER: DX0390K1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-822-7039
? TELEFAX: 201-822-7398
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 323 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? PCT-US94-09642-2

Query Match 11.1%; Score 165.5; DB 5; Length 323;
Best Local Similarity 21.7%; Pred. No. 1.4e-08;
Matches 65; Conservative 61; Mismatches 121; Indels 53; Gaps 13;

QY 3 LGSGLFLFLSSLRADPQEKERVAMVGSDELSCACPEGRDPLNDVYVYMQTSEKTY 62
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 MGLSNILFVM-AFLISGAAPLKIDAYFNETADLPCOPANSONOSLSLVFWQDENLVL 59
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 63 VTYHIFQNSSLENDVSRYYRNFALMSPGMLRGDFSLRLFVNTPODEQKFLVL-LQSLSG 121
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 60 NEVYLGR-EKFDVSHSVYMGRTSFD-----SDSWTLRLNLMLQIKDKLGYCIHHKKPTG 113
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 122 FOEVLSEVTLHVANFSPV-VSAPHSPSODELFTFTCTSINGYPRP-NVYVWINKTDSL 179
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 114 MIRIHMNSELVLANFSOPEIIVISNITENVYINLTCSIHGYPEKKMSVLLRTKNSPT 173
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 180 LD-----QALONDVFLNMGGLDYVSVLRIA--RTPSVNICCIENVLLQONLVGSSQ 231
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 174 IEYDGMKSDOD-----NVTSLDVSISLSVSPDDVSNMTIFCILET----- 216
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 232 TGNDIGERDKITENPVSTGKNA-----ATWSILAVL-----CLVVAVAVAIQW 280
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 217 -----DKTRLSSPFSIELEDPOPPDHPW-ITAVLPVITICVAVFCLIMKMKKKKR 269
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 12
US-08-456-104-2
; Sequence 2, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
```

```

; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; RIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-456-104-2

Query Match      11.1%; Score 165.5; DB 2; Length 329;
Best Local Similarity 21.7%; Pred. No. 1,5e+08;
Matches 65; Conservative 61; Mismatches 121; Indels 53; Gaps 13;

OY    3 LGSPELLFLFFSSLRADTQKEVRAMVGSDEVEISCACPEGSRPDLNDVVYVWOTSSKTY 62
       :|::||:::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     7 MGLSNILFEVM-AFLISGAAPLKIQAYFNENETADLPCCPANSONOSLSELVFWMDQENLVL 65
C      63 VYTHHPONSSLEANDSKRRNRALMSPAGMLRGDFSLFPNVTODEDEKFCGLV-LQSOLG 121
       ::::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     66 NEVYLIGK-EKPDYSKSKMGRTSFD-----SDSWTLRLHLMIQLIKDKLYLCIIHHKKPTG 119
OY    122 FOEVLSEVLTLLHVANESVP-VVSAPHSPSODELTFCTCSINGYPR-NYYWINKTDNSL 179
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     120 MIRHOMNSELSVLANSQPETIVPSINTEWYTNITLCSSIHGYPEKKKSULLRTKNST 179
OY    180 LD-----DALNDTVFLNMRGLYDVSVLRIA--RTPSYNIQCCLENVLLQONTLVSGQ 231
       ::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     180 IEYDGIHQSQD-----NVTELVDVISLSLSPFDVYSNMNTIFCILET----- 222
OY    232 TGNDIGENDKTTEPNVSTGEKNA-----ATWSILAVL-----CLLVVAVALGWCCRDR 280
       ::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     223 -----DKTRLISSFFSIIEEDPPPPDHIPW-TTAAVLPTVIICVWFCLIMWKMKKKR 275

```

```

? TITLE OF INVENTION: NO. 594267el CTLA4/CD28 Ligands and
? TITLE OF INVENTION: uses Therefor
? NUMBER OF SEQUENCES: 25
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD
? STREET: 60 State Street, Suite 510
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/Ms-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/101,624
? FILING DATE: 26-JUL-1993
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Mandragouras, Amy E.
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: RPT-004
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617) 227-7400
? TELEFAX: (617) 227-5941
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 329 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-101-624-2

Query Match      11.1%; Score 165.5; DB 2; Length 329;
Best Local Similarity 21.7%; Pred. No. 1.5e-08;
Matches 65; Conservative 61; Mismatches 121; Indels 53; Gaps 13.

QY   3 LGSPIGLFLFLFSLADNQEKREVRAMVSGDVLSCACPEGSRFDINDVVYMQTSESKT V 62
    :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   7 MLSNILFW-AFLISGAAPLKIQAIFNETADLPQCFANSQMSISELYVFQDDENLVLT 65

QY   63 VTTHIPONSLENDVSRRKRNALMSPAGMLRGDFSLRLFNTPODEQKFCLV-LSQSIG 121
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   66 NEVYLIG-EKEPVSASHKWKGRTSFD-----SDSWTLRLHNLIKKGLAQCIHHKKRPTG 119

QY   122 FOEVLISVEYTLVAANFSVP-VVASAPHSESODELFTCTCSINGIRRP-NVYINKTDSL 179
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   120 MIRIQHMNSELSVLNFSQPEIIVPTSINTENYINLTCSIHGYPEPKMAYLRTKNST 179

QY   180 LD-----QALQNDYFIQMRGLYDVAVSRLA---RTPSVNGCCIEENVLLDONLTVSGS Q 231
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   180 IEYDIQMOSQD-----NTELTLDYSISLSVFPDYVTSMTITFCILET----- 222

QY   232 TGNDIGERDKTIENPVSGEKNA-----ATWSIIAVL-----CLLVAAVAIGNWCRRDR 280
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   223 -----DKTRLSSPFSTILEDPPQPPDHHP-ITAVLPTVIICVWFOLLIMKKKKKKKR 275

RESULT 14
US-08-479-744A-2
? Sequence 2, Application US/08479744A
? Patent No. 6084067
? GENERAL INFORMATION:
? APPLICANT: Freeman, Gordon J.
? APPLICANT: Nadler, Lee M.
? APPLICANT: Gray, Gary S.
? TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
? TITLE OF INVENTION: Uses Therefor
? NUMBER OF SEQUENCES: 35
```


> 0 <
0/10 Intelligenetics
> 0 <

GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Wed 23 Oct 102 14:25:42-PDT

Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Stretching-weight = 1.00
CLUST-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

- 13. US-09-728-420C-17 (1-302)
- 14. US-09-728-420C-18 (1-302)
- 9. US-09-728-420C-12 (1-288)
- 10. US-09-728-420C-13 (1-267)

Region Alignment: (listed in Clustered order)

US-09-728-11 MRGSPGLFLFLFSSLRADTQEKVRAWGSVDVLSQACPEGSRFDLNDVYVYVWQTSSEKT
US-09-728-18 1 MRGSPGLFLFLFSSLRADTQEKVRAWGSVDVLSQACPEGSRFDLNDVYVYVWQTSSEKT
US-09-728-12 1 MRGSPGLFLFLFSSLRADTQEKVRAWGSVDVLSQACPEGSRFDLNDVYVYVWQTSSEKT
US-09-728-13 1 MRGSPGLFLFLFSSLRADTQEKVRAWGSVDVLSQACPEGSRFDLNDVYVYVWQTSSEKT
consensus mr1gspglflflfsslradtqekvramwgsdvelscacpegSRFDLNDVYVYVWQTSSEKT

US-09-728-62 VVYTHIPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLEFNVTPODEQKFHCLVLSQSLGF
US-09-728-62 VVYTHIPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLEFNVTPODEQKFHCLVLSQSLGF
US 728-62 VVYTHIPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLEFNVTPODEQKFHCLVLSQSLGF
US-09-728-41 VVYTHIPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLEFNVTPODEQKFHCLVLSQSLGF
consensus VVYTHIPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLEFNVTPODEQKFHCLVLSQSLGF

US-09-728-123 QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA
US-09-728-123 QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA
US-09-728-123 QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA
US-09-728-102 QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA
US-09-728-102 QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA
consensus QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA

US-09-728-184 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIQCCIEENVLLQONLTVGSQGTGNDIGERDKITE
US-09-728-184 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIQCCIEENVLLQONLTVGSQGTGNDIGERDKITE
US-09-728-184 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIQCCIEENVLLQONLTVGSQGTGNDIGERDKITE
US-09-728-184 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIQCCIEENVLLQONLTVGSQGTGNDIGERDKITE

US-09-728-163 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIQCCIEENVLLQONLTVGSQGTGNDIGERDKITE
consensus LQNDTVFLNMRGLYDVVSVLRIARTPSVNIQCCIEENVLLQONLTVGSQGTGNDIGERDKITE
US-09-728-245 NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRRDRCLOHSHYAGAMAVSPETELTGHV
US-09-728-245 NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRRDRCLOHSHYAGAMAVSPETELTGHV
US-09-728-245 NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRRDRCLOHSHYAG
US-09-728-224 NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRRDRCLOHSHYAG
consensus NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRRDRCLOHSHYAGAMAVSPETELTGHV

Alignment score = 612.00

Scoring matrix:

	9	10	13	14
9	162	218	218	
10		92	92	
13			302	
14				

